(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(43) International Publication Date
21 September 2000 (21.09.2000)

PCT

(10) International Publication Number
WO 00/55375 A1

(51) International Patent Classification[7]:
C12Q 1/68, C12N 15/00, 15/09, 15/63, 15/86

(21) International Application Number:
PCT/US00/07285

(22) International Filing Date:
17 March 2000 (17.03.2000)

(25) Filing Language: English

(26) Publication Language:

(30) Priority Data

60/124,916	17 March 1999 (17.03.1999)	US
60/124,808	17 March 1999 (17.03.1999)	US
60/149,639	17 August 1999 (17.08.1999)	US
60/157,247	01 October 1999 (01.10.1999)	US
60/167,824	29 November 1999 (29.11.1999)	US
60/182,711	15 February 2000 (15.02.2000)	US

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(81) Designated States (national): AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG)

Published

-- *with international search report*

-- *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments*

(54) Title: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

(57) Abstract
Novel polynucleotides and the proteins encoded thereby are disclosed.

SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM This application is a continuation-in-part of the following applications: (1) provisional application Ser. No. 60/124,916, filed March 17,1999; (2) provisional application Ser. No. 60/124,808, filed March 17,1999; (3) provisional application Ser. No. 60/149,639, filed August 17,1999; (4) provisional application Ser. No. 60/157,247, filed October 1,1999; (5) provisional application Ser. No. 60/167,824, filed November 29,1999; (6) provisional application Ser. No. 60/182,711, filed February 15,2000; all of which are incorporated by reference herein.

FIELD OF THE INVENTION The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins.

BACKGROUND OF THE INVENTION Technology aimed at the discovery of protein factors (including e. g., cytokines, such as lymphokines, interferons, CSFs and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides"directly"in the sense that they rely on information directly related to the discovered protein (i. e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent"indirect"cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity by virtue of their secreted nature in the case of leader sequence cloning, or by virtue of the cell or tissue source in the case of PCR-based techniques. It is to these proteins and the polynucleotides encoding them that the present invention is directed.

SUMMARY OF THE INVENTION In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 1; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 1 from nucleotide 27 to nucleotide 260; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 1 from nucleotide 72 to nucleotide 260; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number 207114; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number 207114; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number 207114; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number 207114; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 2; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 2 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 2; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least of the length of SEQ ID NO:

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO: 1 from nucleotide 27 to nucleotide 260; the nucleotide sequence of SEQ ID NO: from nucleotide 72 to nucleotide 260; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 2, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 2 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID 2.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO:

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (aa) SEQ ID NO: but excluding the poly (A) tail at the 3'end of SEQ ID NO: and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number 207114; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (ba) SEQ ID NO: 1, but excluding the poly (A) tail at the 3'end of SEQ ID 1; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number 207114; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID NO: 1, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID NO: 1 to a nucleotide sequence corresponding to the 3'end of SEQ ID NO: 1, but excluding the poly (A) tail at the 3'end of SEQ ID 1. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID NO: 1 from nucleotide 27 to nucleotide 260, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 1 from nucleotide 27 to nucleotide 260, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 1 from nucleotide 27 to nucleotide 260. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID from nucleotide 72 to nucleotide 260, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID NO: 1 from nucleotide 72 to nucleotide 260, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID NO: 1 from nucleotide 72 to nucleotide 260.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 2; (b) a fragment of the amino acid sequence of SEQ ID 2, the fragment comprising eight contiguous amino acids of SEQ ID 2; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number 207114; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 2. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 2 having biological activity, the fragment preferably comprising

eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 2, or a protein comprising a fragment of the amino acid sequence of SEQ ID 2 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID 2.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 3; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 3 from nucleotide 6 to nucleotide 1325; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 3 from nucleotide 99 to nucleotide 1325; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number 207114; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone vpl0_1 deposited with the ATCC under accession number 207114; protein coding sequence of clone vpl0_1 deposited with the ATCC under accession number 207114; (g) a polynucleotide encoding a mature protein encoded by the insert of clone vpl0_1 deposited with the ATCC under accession number 207114; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 4; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 4 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 4; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID 3.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 3 from nucleotide 6 to nucleotide 1325; the nucleotide sequence of 3 from nucleotide 99 to nucleotide 1325; the nucleotide sequence of the full-length protein coding sequence of clone vpl0_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 4, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 4 having biological activity, the fragment comprising the amino acid sequence from amino acid 215 to amino acid 224 of SEQ ID 4.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 3.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID 3, but excluding the poly (A) tail at the 3'end of SEQ ID 3; and (ab) the nucleotide sequence of the insert of clone vp deposited with the ATCC under accession number 207114; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID 3, but excluding the poly (A) tail at the 3'end of SEQ ID 3; and (bb) the nucleotide sequence of the insert of clone vp deposited with the ATCC under accession number 207114; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii). Preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 3, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 3 to a nucleotide sequence corresponding to the 3'end of SEQ ID 3, but excluding the poly (A) tail at the 3'end of SEQ ID 3. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 3 from nucleotide 6 to nucleotide 1325, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 3 from nucleotide 6 to nucleotide 1325, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 3 from nucleotide 6 to nucleotide 1325. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 3 from nucleotide 99 to nucleotide 1325, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 3 from nucleotide 99 to nucleotide 1325, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 3 from nucleotide 99 to nucleotide 1325.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 4; (b) a fragment of the amino acid sequence of SEQ ID 4, the fragment comprising eight contiguous amino acids of SEQ ID 4; and the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number 207114; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 4. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 4, or a protein comprising a fragment of the amino acid sequence of SEQ ID 4 having biological activity, the fragment comprising the amino acid sequence from amino acid 215 to amino acid 224 of SEQ ID 4.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 5 from nucleotide 149 to nucleotide 322; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID from nucleotide 200 to nucleotide 322; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone vpl deposited with the ATCC under accession number 207114; (e) a polynucleotide encoding the protein encoded by the insert of clone vpl 1_1 deposited with the ATCC under accession number 207114; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number 207114; (g) a polynucleotide encoding a mature protein encoded by the insert of clone vpl 1_1 deposited with the ATCC under accession number 207114; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 6; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 6 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 6; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID from nucleotide 149 to nucleotide 322; the nucleotide sequence of SEQ ID from nucleotide 200 to nucleotide 322; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vpl deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with

the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 6, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 6 having biological activity, the fragment comprising the amino acid sequence from amino acid 24 to amino acid 33 of SEQ ID 6.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO:

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID but excluding the poly (A) tail at the 3'end of SEQ ID and (ab) the nucleotide sequence of the insert of clone vpl 1_1 deposited with the ATCC under accession number 207114; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID but excluding the poly (A) tail at the 3'end of SEQ ID and (bb) the nucleotide sequence of the insert of clone vp deposited with the ATCC under accession number 207114; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 5, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID to a nucleotide sequence corresponding to the 3'end of SEQ ID but excluding the poly (A) tail at the 3'end of SEQ ID Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 5 from nucleotide 149 to nucleotide 322, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID from nucleotide 149 to nucleotide 322, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID from nucleotide 149 to nucleotide 322. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID from nucleotide 200 to nucleotide 322, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 5 from nucleotide 200 to nucleotide 322, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 5 from nucleotide 200 to nucleotide 322.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 6; (b) a fragment of the amino acid sequence of SEQ ID 6, the fragment comprising eight contiguous amino acids of SEQ ID 6; and (c) the amino acid sequence encoded by the insert of clone vpl 1_1 deposited with the ATCC under accession number 207114; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 6. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 6, or a protein comprising a fragment of the amino acid sequence of SEQ ID 6 having biological activity, the fragment comprising the amino acid sequence from amino acid 24 to amino acid 33 of SEQ ID 6.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ

ID 7; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 7 from nucleotide 288 to nucleotide 629; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 7 from nucleotide 363 to nucleotide 629; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone vpl3_1 deposited with the ATCC under accession number 207114; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone vpl3_1 deposited with the ATCC under accession number 207114; protein coding sequence of clone vpl3_1 deposited with the ATCC under accession number 207114; (g) a polynucleotide encoding a mature protein encoded by the insert of clone vp deposited with the ATCC under accession number 207114; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 8; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 8 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 8; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID 7.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 7 from nucleotide 288 to nucleotide 629; the nucleotide sequence of SEQ ID 7 from nucleotide 363 to nucleotide 629; the nucleotide sequence of the full-length protein coding sequence of clone vpl3_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone vpl3_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 8, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 8 having biological activity, the fragment comprising the amino acid sequence from amino acid 52 to amino acid 61 of SEQ ID 8.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 7.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID 7, but excluding the poly (A) tail at the 3'end of SEQ ID 7; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number 207114; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (ba) SEQ ID 7, but excluding the poly (A) tail at the 3'end of SEQ ID 7; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number 207114; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii). Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID N0: 7, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 7 to a nucleotide sequence corresponding to the 3'end of SEQ ID 7, but excluding the poly (A) tail at the 3'end of SEQ ID 7. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ

ID 7 from nucleotide 288 to nucleotide 629, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 7 from nucleotide to nucleotide 629, to a nucleotide sequence nucleotide 629. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 7 from nucleotide 363 to nucleotide 629, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 7 from nucleotide 363 to nucleotide 629, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 7 from nucleotide 363 to nucleotide 629.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (b) a fragment of the amino acid sequence of SEQ ID 8, the fragment comprising eight contiguous amino acids of SEQ ID 8; and (c) the amino acid sequence encoded by the insert of clone vpl3_1 deposited with the ATCC under accession number 207114; the protein being substantially free from other mammalian proteins. Preferably such embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids amino acid 52 to amino acid 61 of SEQ ID 8.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 9; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 9 from nucleotide 11 to nucleotide 298; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 9 from nucleotide 149 to nucleotide 298; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone vpl6_1 deposited with the ATCC under accession number 207114; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone vpl6_1 deposited with the ATCC under accession number 207114; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vpl6_1 deposited with the ATCC under accession number 207114; (g) a polynucleotide encoding a mature protein encoded by the insert of clone vpl6_1 deposited with the ATCC under accession number 207114; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO: 10; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 10 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 10; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID 9.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 9 from nucleotide 11 to nucleotide 298; the nucleotide sequence of 9 from nucleotide 149 to nucleotide 298; the nucleotide sequence sequence of clone vp 16_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone vpl6_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO: 10, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 10 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO: 10.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 9.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of : (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID 9, but excluding the poly (A) tail at the 3'end of SEQ ID 9; and (ab) the nucleotide sequence of the insert of clone vp deposited with the ATCC under accession number 207114; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe(s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (ba) SEQ ID 9, but excluding the poly (A) tail at the 3'end of SEQ ID 9; and (bb) the nucleotide sequence of the insert of clone vp deposited with the ATCC under accession number 207114; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 9, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 9 to a nucleotide sequence corresponding to the 3'end of SEQ ID 9, but excluding the poly (A) tail at the 3'end of SEQ ID 9. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 9 from nucleotide 11 to nucleotide 298, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 9 from nucleotide 11 to nucleotide 298, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 9 from nucleotide 11 to nucleotide 298. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 9 from nucleotide 149 to nucleotide 298, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 9 from nucleotide 149 to nucleotide 298, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 9 from nucleotide 149 to nucleotide 298.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID NO: 10; (b) a fragment of the amino acid sequence of SEQ ID 10, the fragment comprising eight contiguous amino acids of SEQ ID NO: 10; and (c) the amino acid sequence encoded by the insert of clone vpl6_1 deposited with the ATCC under accession number 207114; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 10. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO: 10, or a protein comprising a fragment of the amino acid sequence of SEQ ID 10 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO: 10.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 11; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 11 from nucleotide 257 to nucleotide 607; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 11 from nucleotide 479 to nucleotide 607; (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp21_1 deposited with the ATCC under accession number 207114; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone vp21_1 deposited with the ATCC under accession number 207114; protein coding sequence of clone vp21_1 deposited with the ATCC under accession number 207114; (g) a polynucleotide encoding a mature protein encoded by the insert of clone vp21_1 deposited with the ATCC under accession number

207114; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 12; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 12 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 12; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID NO:

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO: 11 from nucleotide 257 to nucleotide 607; the nucleotide sequence of SEQ ID NO: from nucleotide 479 to nucleotide 607; the nucleotide sequence of the full-length protein coding sequence of clone vp21_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vp21_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone vp21_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO: 12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 12, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 12 having biological activity, the fragment comprising the amino acid sequence from amino acid 53 to amino acid 62 of SEQ ID 12.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 11.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting (a) a process comprising the steps (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (aa) SEQ ID NO: 11, but excluding the poly (A) tail at the 3'end of SEQ ID NO: 11; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number 207114; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (ba) SEQ ID NO: 11, but excluding the poly (A) tail at the 3'end of SEQ ID NO: 11; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number 207114; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii). Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 11, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 11 to a nucleotide sequence corresponding to the 3'end of SEQ ID 11, but excluding the poly (A) tail at the 3'end of SEQ ID 11. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID NO: 11 from nucleotide 257 to nucleotide 607, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID NO: 11 from nucleotide 257 to nucleotide 607, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID NO: 11 from nucleotide 257 to nucleotide 607. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 11 from nucleotide 479 to nucleotide 607, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID NO: 11 from nucleotide 479 to nucleotide 607, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID NO: 11 from nucleotide

479 to nucleotide 607.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 12; (b) a fragment of the amino acid sequence of SEQ ID 12, the fragment comprising eight contiguous amino acids of SEQ ID 12; and (c) the amino acid sequence encoded by the insert of clone vp21_1 deposited with the ATCC under accession number 207114; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 12. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO: 12, or a protein comprising a fragment of the amino acid sequence of SEQ ID 12 having biological activity, the fragment comprising the amino acid sequence from amino acid 53 to amino acid 62 of SEQ ID NO: 12.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 13; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 13 from nucleotide 163 to nucleotide 477; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 13 from nucleotide 238 to nucleotide 477; (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp22_1 deposited with the ATCC under accession number 207114; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number 207114; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp22_1 deposited with the ATCC under accession number 207114; (g) a polynucleotide encoding a mature protein encoded by the insert of clone vp22_1 deposited with the ATCC under accession number 207114; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO: 14; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 14 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO: 14; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least of the length of SEQ ID 13.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO: 13 from nucleotide 163 to nucleotide 477; the nucleotide sequence of SEQ ID NO: 13 from nucleotide 238 to nucleotide 477; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO: 14 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO: 14, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 14 having biological activity, the fragment comprising the amino acid sequence from amino acid 47 to amino acid 56 of SEQ ID NO: 14.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 13.

Further embodiments of the invention provide isolated polynucleotides produced according to a process

selected from the group consisting (a) a process comprising the steps (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (aa) SEQ ID 13, but excluding the poly (A) tail 3'end of SEQ ID 13; and (ab) the nucleotide sequence of the insert of clone vp22_1 deposited with the ATCC under accession number 207114; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe(s); and (b) a process comprising the steps (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID NO: 13, but excluding the poly (A) tail at the 3'end of SEQ ID 13; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number 207114; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 13, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 13 to a nucleotide sequence corresponding to the 3'end of SEQ ID 13, but excluding the poly (A) tail at the 3'end of SEQ ID 13. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID NO: 13 from nucleotide 163 to nucleotide 477, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID NO: 13 from nucleotide 163 to nucleotide 477, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID NO: 13 from nucleotide 163 to nucleotide 477. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 13 from nucleotide 238 to nucleotide 477, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 13 from nucleotide to nucleotide 477, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID NO: 13 from nucleotide 238 to nucleotide 477.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID NO: 14; (b) a fragment of the amino acid sequence of SEQ ID 14, the fragment comprising eight contiguous amino acids of SEQ ID NO: 14; and (c) the amino acid sequence encoded by the insert of clone vp22_1 deposited with the ATCC under accession number 207114; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 14. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 14 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO: 14, or a protein comprising a fragment of the amino acid sequence of SEQ ID 14 having biological activity, the fragment comprising the amino acid sequence from amino acid 47 to amino acid 56 of SEQ ID NO: 14.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 15; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 15 from nucleotide 58 to nucleotide 624; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 15 from nucleotide 106 to nucleotide 624; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number 207114; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number 207114; protein coding sequence of clone vq2_1 deposited with the ATCC under accession number 207114; (g) a polynucleotide encoding a mature protein encoded by the insert of clone vq2_1 deposited with the ATCC under accession number 207114; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO: 16; (i) a polynucleotide encoding a

protein comprising a fragment of the amino acid sequence of SEQ ID 16 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO: 16; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID NO: 15.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 15 from nucleotide 58 to nucleotide 624; the nucleotide sequence of SEQ ID 15 from nucleotide 106 to nucleotide 624; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vq2_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO: 16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 16, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 16 having biological activity, the fragment comprising the amino acid sequence from amino acid 89 to amino acid 98 of SEQ ID 16.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 15.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (aa) SEQ ID NO: 15, but excluding the poly (A) tail at the 3'end of SEQ ID 15; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number 207114; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe(s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID NO: 15, but excluding the poly (A) tail at the 3'end of SEQ ID NO: 15; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number 207114; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 15, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 15 to a nucleotide sequence corresponding to the 3'end of SEQ ID 15, but excluding the poly (A) tail at the 3'end of SEQ ID 15. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID NO: 15 from nucleotide 58 to nucleotide 624, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID NO: 15 from nucleotide 58 to nucleotide 624, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID NO: 15 from nucleotide 58 to nucleotide 624. Also preferably the polynucleotide isolated according to the above nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID NO: 15 from nucleotide 106 to nucleotide 624, to a nucleotide sequence corresponding to the 3'end of

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid

sequence of SEQ ID NO: 16; fragment comprising eight contiguous amino acids of SEQ ID 16; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number 207114; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 16. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO: 16, or a protein comprising a fragment of the amino acid sequence of SEQ ID 16 having biological activity, the fragment comprising the amino acid sequence from amino acid 89 to amino acid 98 of SEQ ID 16.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 17; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 17 from nucleotide 773 to nucleotide 1090; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 17 from nucleotide 842 to nucleotide 1090; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number 207114; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number 207114; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number 207114; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number 207114; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO: 18; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 18 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO: 18; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID 17.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO: 17 from nucleotide 773 to nucleotide 1090; the nucleotide sequence of SEQ ID NO: 17 from nucleotide 842 to nucleotide 1090; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vq3_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO: 18 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 18, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 18 having biological activity, the fragment comprising the amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID NO: 18.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 17.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID NO: 17, but excluding the poly (A) tail at the 3'end of SEQ ID NO: 17; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number 207114; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as

stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (ba) SEQ ID NO: 17, but excluding the poly (A) tail at the 3'end of SEQ ID NO: 17; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number 207114; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 17, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 17 to a nucleotide sequence corresponding to the 3'end of SEQ ID 17, but excluding the poly (A) tail at the 3'end of SEQ ID 17. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID NO: 17 from nucleotide 773 to nucleotide 1090, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID NO: 17 from nucleotide 773 to nucleotide 1090, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID NO: 17 from nucleotide 773 to nucleotide 1090. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 17 from nucleotide 842 to nucleotide 1090, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID NO: 17 from nucleotide 842 to nucleotide 1090, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 17 from nucleotide 842 to nucleotide 1090.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 18; (b) a fragment of the amino acid sequence of SEQ ID 18, the fragment comprising eight contiguous amino acids of SEQ ID 18; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number 207114; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 18. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 18 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO: 18, or a protein comprising a fragment of the amino acid sequence of SEQ ID 18 having biological activity, the fragment comprising the amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID 18.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 19; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 19 from nucleotide 96 to nucleotide 275; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 19 from nucleotide 159 to nucleotide 275; (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq5_1 deposited with the ATCC under accession number 207114; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number 207114; protein coding sequence of clone deposited with the ATCC under accession number 207114; (g) a polynucleotide encoding a mature protein encoded by the insert of clone vq5_1 deposited with the ATCC under accession number 207114; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 20; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 20 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 20; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the

protein of (h) or (i) above; a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID 19.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO: 19 from nucleotide 96 to nucleotide 275; the nucleotide sequence of SEQ ID NO: 19 from nucleotide 159 to nucleotide 275; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 20, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 20 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID 20.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 19.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID NO: 19, but excluding the poly (A) tail at the 3'end of SEQ ID 19; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number 207114; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID NO: 19, but excluding the poly (A) tail at the 3'end of SEQ ID 19; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number 207114; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii). Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 19, and excluding the poly (A) tail at the 3'end of SEQ ID 19. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID NO: 19 from nucleotide 96 to nucleotide 275, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID NO: 19 from nucleotide 96 to nucleotide 275, to a nucleotide 96 to nucleotide 275. Also preferably the polynucleotide isolated according to the above nucleotide 159 to nucleotide 275, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID NO: 19 from nucleotide 159 to nucleotide 275.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 20; fragment comprising eight contiguous amino acids of SEQ ID 20; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number 207114; the protein being substantially free from other mammalian proteins. Preferably such embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids ID 20 having biological activity, the

fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID 20.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 21; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 21 from nucleotide 176 to nucleotide 340; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 21 from nucleotide 230 to nucleotide 340; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number 207114; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number 207114; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number 207114; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number 207114; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 22; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 22 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 22; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID 21.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 21 from nucleotide 176 to nucleotide 340; the nucleotide sequence of SEQ ID 21 from nucleotide 230 to nucleotide 340; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vq6_l deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 22 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 22, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 22 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID 22.

Other embodiments provide the gene corresponding to the sequence of SEQ ID 21.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID but excluding the poly (A) tail at the 3'end of SEQ ID and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number 207114; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID but excluding the poly (A) tail at the 3'end of SEQ ID and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number 207114; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

corresponding to the sequence of SEQ ID 21, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 21 to a nucleotide sequence corresponding to the 3'end of SEQ ID 21, but excluding the poly (A) tail at the 3'end of SEQ ID 21. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 21 from nucleotide 176 to nucleotide 340, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 21 from nucleotide 176 to nucleotide 340, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 21 from nucleotide 176 to nucleotide 340. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 21 from nucleotide 230 to nucleotide 340, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 21 from nucleotide 230 to nucleotide 340, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 21 from nucleotide 230 to nucleotide 340.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 22; (b) a fragment of the amino acid sequence of SEQ ID 22, the fragment comprising eight contiguous amino acids of SEQ ID 22; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number 207114; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 22. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 22 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 22, or a protein comprising a fragment of the amino acid sequence of SEQ ID 22 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID 22.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 23; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 23 from nucleotide 29 to nucleotide 1111; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 23 from nucleotide 167 to nucleotide 1111; (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number 207114; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone vrl_1 deposited with the ATCC under accession number 207114; protein coding sequence of clone deposited with the ATCC under accession number 207114; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number 207114; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 24; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 24 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 24; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID NO: 23.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 23 from nucleotide 29 to nucleotide 1111; the nucleotide sequence of SEQ ID 23 from nucleotide 167 to nucleotide 1111; the nucleotide sequence of the full-length protein coding sequence of clone vrl_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone vrl_1 deposited

with the ATCC under accession number 207114.

In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 24, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 24 having biological activity, the fragment comprising the amino acid sequence from amino acid 175 to amino acid 184 of SEQ ID 24.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 23.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID 23, but excluding the poly (A) tail at the 3'end of SEQ ID 23; and (ab) the nucleotide sequence of the insert of clone vrl_1 deposited with the ATCC under accession number 207114; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID 23, but excluding the poly (A) tail at the 3'end of SEQ ID 23; and (bb) the nucleotide sequence of the insert of clone vrl_1 deposited with the ATCC under accession number 207114; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 23, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 23 to a nucleotide sequence corresponding to the 3'end of SEQ ID 23, but excluding the poly (A) tail at the 3'end of SEQ ID 23. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 23 from nucleotide 29 to nucleotide 1111, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 23 from nucleotide 29 to nucleotide 1111, to a nucleotide 29 to nucleotide 1111. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 23 from nucleotide 167 to nucleotide 1111, and extending contiguously from a nucleotide 167 to nucleotide 1111, to a nucleotide sequence corresponding to the 3'end

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 24; fragment comprising eight contiguous amino acids of SEQ ID 24; and (c) the amino acid sequence encoded by the insert of clone vrl_1 deposited with the ATCC under accession number 207114; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 24. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 24, or a protein comprising a fragment of the amino acid sequence of SEQ ID 24 having biological activity, the fragment comprising the amino acid sequence from amino acid 175 to amino acid 184 of SEQ ID 24.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide

selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 25; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 25 from nucleotide 13 to nucleotide 513; (c) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number 207115; (d) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number 207115; (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number 207115; a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number 207115; (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 26; (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 26 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 26; (i) a polynucleotide which is an allelic variant of a polynucleotide of above; a polynucleotide which encodes a species homologue of the protein of (g) or (h) above; (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in and (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in and that has a length that is at least 25% of the length of SEQ ID NO: 25.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 25 from nucleotide 13 to nucleotide 513; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number 207115; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number 207115. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number 207115. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 26 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 26, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 26 having biological activity, the fragment comprising the amino acid sequence from amino acid 78 to amino acid 87 of SEQ ID 26.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 25.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting SEQ ID 25, but excluding the poly (A) tail at the 3'end of SEQ ID 25; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number 207115; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID 25, but excluding the poly (A) tail at the 3'end of SEQ ID 25; and (bb) the nucleotide sequence of the insert of clone the ATCC under accession number 207115; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 25, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 25 to a nucleotide sequence corresponding to the 3'end of SEQ ID 25, but excluding the poly (A) tail at the 3'end of SEQ ID 25. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence

of SEQ ID 25 from nucleotide 13 to nucleotide 513, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 25 from nucleotide 13 to nucleotide 513, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 25 from nucleotide 13 to nucleotide 513.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 26; (b) a fragment of the amino acid sequence of SEQ ID 26, the fragment comprising eight contiguous amino acids of SEQ ID 26; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number 207115; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 26. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 26 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 26, or a protein comprising a fragment of the amino acid sequence of SEQ ID 26 having biological activity, the fragment comprising the amino acid sequence from amino acid 78 to amino acid 87 of SEQ ID 26.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 27; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 27 from nucleotide 79 to nucleotide 345; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 27 from nucleotide 130 to nucleotide 345; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone vb25_1 deposited with the ATCC under accession number PTA-362; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 362; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 28; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 28 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 28; (j) a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID NO: 27.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 27 from nucleotide 79 to nucleotide 345; the nucleotide sequence of SEQ ID 27 from nucleotide 130 to nucleotide 345; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA- 362; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 28, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 28 having biological activity, the fragment comprising the amino acid sequence from amino acid 39 to amino acid 48 of SEQ ID 28.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 27.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID 27, but excluding the poly (A) tail at the 3'end of SEQ ID 27; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 362; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe(s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID 27, but excluding the poly (A) tail at the 3'end of SEQ ID 27; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 362; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 27, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 27 to a nucleotide sequence corresponding to the 3'end of SEQ ID 27, but excluding the poly (A) tail at the 3'end of SEQ ID 27. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 27 from nucleotide 79 to nucleotide 345, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 27 from nucleotide 79 to nucleotide 345, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 27 from nucleotide 79 to nucleotide 345. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 27 from nucleotide 130 to nucleotide 345, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 27 from nucleotide 130 to nucleotide 345, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 27 from nucleotide 130 to nucleotide 345.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 28; (b) a fragment of the amino acid sequence of SEQ ID 28, the fragment comprising eight contiguous amino acids of SEQ ID 28; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 28. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 28, or a protein comprising a fragment of the amino acid sequence of SEQ ID 28 having biological activity, the fragment comprising the amino acid sequence from amino acid 39 to amino acid 48 of SEQ ID 28.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 29; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 29 from nucleotide 72 to nucleotide 236; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 29 from nucleotide 150 to nucleotide 236; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; a polynucleotide comprising the nucleotide sequence of a mature

protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (g) a polynucleotide encoding a mature protein encoded by the insert of clone vb27_1 deposited with the ATCC under accession number PTA- 362; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 30; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 30 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 30; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID 29.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 29 from nucleotide 72 to nucleotide 236; the nucleotide sequence of SEQ ID 29 from nucleotide 150 to nucleotide 236; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA- 362; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number 362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 30, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 30 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID 30.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 29.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (aa) SEQ ID NO: 29, but excluding the poly (A) tail at the 3'end of SEQ ID 29; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 362; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (ba) SEQ ID 29, but excluding the poly (A) tail at the 3'end of SEQ ID 29; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 362; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 29, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 29 to a nucleotide sequence corresponding to the 3'end of SEQ ID 29, but excluding the poly (A) tail at the 3'end of SEQ ID 29. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 29 from nucleotide 72 to nucleotide 236, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 29 from nucleotide 72 to nucleotide 236, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 29 from nucleotide 72 to nucleotide 236. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 29 from nucleotide 150 to nucleotide 236, and extending contiguously from a nucleotide sequence corresponding to the 5'end of

said sequence of SEQ ID 29 from nucleotide 150 to nucleotide 236, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 29 from nucleotide 150 to nucleotide 236.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 30; (b) a fragment of the amino acid sequence of SEQ ID 30, the fragment comprising eight contiguous amino acids of SEQ ID 30; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 30. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 30, or a protein comprising a fragment of the amino acid sequence of SEQ ID 30 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID 30.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 31; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 31 from nucleotide 135 to nucleotide 884; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 31 from nucleotide 183 to nucleotide 884; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone vb28_1 deposited with the ATCC under accession number PTA-362; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone vb28_1 deposited with the ATCC under accession number PTA-362; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 362; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 32; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 32 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 32; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in and that has a length that is at least of the length of SEQ ID

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID from nucleotide to nucleotide the nucleotide sequence of SEQ ID from nucleotide 183 to nucleotide 884; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA- 362; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 32, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 32 having biological activity, the fragment comprising the amino acid sequence from amino acid 120 to amino acid 129 of SEQ ID 32.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO:

Further embodiments of the invention provide isolated polynucleotides produced according to a process

selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of : (aa) SEQ ID NO: but excluding the poly (A) tail at the 3'end of SEQ ID and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 362; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (ba) SEQ ID but excluding the poly (A) tail at the 3'end of SEQ ID and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 362; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 31 to a nucleotide sequence corresponding to the 3'end of SEQ ID 31, but excluding the poly (A) tail at the 3'end of SEQ ID 31. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 31 from nucleotide 135 to nucleotide 884, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 31 from nucleotide 135 to nucleotide 884, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 31 from nucleotide 135 to nucleotide 884. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 31 from nucleotide 183 to nucleotide 884, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 31 from nucleotide 183 to nucleotide 884, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 31 from nucleotide 183 to nucleotide 884.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 32; (b) a fragment of the amino acid sequence of SEQ ID 32, the fragment comprising eight contiguous amino acids of SEQ ID 32; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 32. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 32, or a protein comprising a fragment of the amino acid sequence of SEQ ID 32 having biological activity, the fragment comprising the amino acid sequence from amino acid 120 to amino acid 129 of SEQ ID 32.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 33; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 33 from nucleotide 42 to nucleotide 206; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 33 from nucleotide 111 to nucleotide 206; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone vb29_1 deposited with the ATCC under accession number PTA-362; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (g) a polynucleotide encoding a mature protein encoded by the insert of clone vb29_1 deposited with the ATCC under accession number PTA- 362; (h) a polynucleotide encoding a protein comprising the

amino acid sequence of SEQ ID 34; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 34 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 34; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID NO: 33.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 33 from nucleotide 42 to nucleotide 206; the nucleotide sequence of SEQ ID 33 from nucleotide 111 to nucleotide 206; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA- 362; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 34, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 34 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID 34.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 33.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID 33, but excluding the poly (A) tail at the 3'end of SEQ ID 33; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 362; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe(s); and (b) a process comprising the steps in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (ba) SEQ ID 33, but excluding the poly (A) tail at the 3'end of SEQ ID 33; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 362; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 33, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 33 to a nucleotide sequence corresponding to the 3'end of SEQ ID 33, but excluding the poly (A) tail at the 3'end of SEQ ID 33. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID from nucleotide 42 to nucleotide 206, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 33 from nucleotide 42 to nucleotide 206, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 33 from nucleotide 42 to nucleotide 206. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 33 from nucleotide 111 to nucleotide 206, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 33 from nucleotide 111 to nucleotide 206, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 33 from nucleotide 111 to nucleotide 206.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 34; (b) a fragment of the amino acid sequence of SEQ ID 34, the fragment comprising eight contiguous amino acids of SEQ ID 34; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 34. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 34, or a protein comprising a fragment of the amino acid sequence of SEQ ID 34 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID 34.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 35; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 35 from nucleotide 17 to nucleotide 253; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 35 from nucleotide 98 to nucleotide 253; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone vb30_1 deposited with the ATCC under accession number PTA-362; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 362; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 36; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 36 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 36; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID NO: 35.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 35 from nucleotide 17 to nucleotide 253; the nucleotide sequence of SEQ ID 35 from nucleotide 98 to nucleotide 253; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA- 362; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone vb30_1 deposited with the ATCC under accession number PTA- 362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 36 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 36, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 36 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID 36.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 35.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more

polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID but excluding the poly (A) tail at the 3'end of SEQ ID 35; and the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 362; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID 35, but excluding the poly (A) tail at the 3'end of SEQ ID and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 362; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 35, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID excluding the poly (A) tail at the 3'end of SEQ ID 35. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 35 from nucleotide 17 to nucleotide 253, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 35 from nucleotide 17 to nucleotide 253, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 35 from nucleotide 17 to nucleotide 253. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 35 from nucleotide 98 to nucleotide 253, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 35 from nucleotide 98 to nucleotide 253.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (b) a fragment of the amino acid sequence of SEQ ID 36, the fragment comprising eight contiguous amino acids of SEQ ID 36; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 36. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID or a protein comprising a fragment of the amino acid sequence of SEQ ID 36 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID 36.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 37; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 37 from nucleotide 68 to nucleotide 424; (c) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (d) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362; a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 362; (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 38; (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 38 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 38; (i) a polynucleotide which is an allelic variant of a polynucleotide of above; a polynucleotide which encodes a species homologue of the protein of (g) or (h) above; (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in

and (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in and that has a length that is at least 25% of the length of SEQ ID 37.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 37 from nucleotide 68 to nucleotide 424; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 38 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 38, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 38 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID 38.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 37.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (aa) SEQ ID 37, but excluding the poly (A) tail 3'end of SEQ ID 37; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 362; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID 37, but excluding the poly (A) tail at the 3'end of SEQ ID 37; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 362; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 37, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 37 to a nucleotide sequence corresponding to the 3'end of SEQ ID 37, but excluding the poly (A) tail at the 3'end of SEQ ID 37. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 37 from nucleotide 68 to nucleotide 424, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 37 from nucleotide 68 to nucleotide 424, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 37 from nucleotide 68 to nucleotide 424.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 38; (b) a fragment of the amino acid sequence of SEQ ID 38, the fragment comprising eight contiguous amino acids of SEQ ID 38; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 38. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 38 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino

acids of SEQ ID 38, or a protein comprising a fragment of the amino acid sequence of SEQ ID 38 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID 38.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 39; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 39 from nucleotide 103 to nucleotide 261; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 39 from nucleotide 154 to nucleotide 261; (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 40; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 40 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 40; (j) a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ 39.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 39 from nucleotide 103 to nucleotide 261; the nucleotide sequence of SEQ ID 39 from nucleotide 154 to nucleotide the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA- 362; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone vf4_1 deposited with the ATCC under accession number PTA- 362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 40 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 40, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 40 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID 40.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 39.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID 39, but excluding the poly (A) tail at the 3'end of SEQ ID and (ab) the nucleotide sequence of the insert of clone vf4_1 deposited with the ATCC under accession number PTA-362; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe(s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID 39, but excluding the poly (A) tail 3'end of SEQ ID 39; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA-362; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 39, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 39 to a nucleotide sequence corresponding to the 3'end of SEQ ID 39, but excluding the poly (A) tail at the 3'end of SEQ ID 39. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID from nucleotide 103 to nucleotide and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 39 from nucleotide 103 to nucleotide 261, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 39 from nucleotide 103 to nucleotide 261. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 39 from nucleotide 154 to nucleotide 261, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 39 from nucleotide 154 to nucleotide to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 39 from nucleotide 154 to nucleotide 261.

In other embodiments, the present invention provides a composition comprising protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 40; (b) a fragment of the amino acid sequence of SEQ ID 40, the fragment comprising eight contiguous amino acids of SEQ ID 40; and (c) the amino acid sequence encoded by the insert of clone vf4_1 deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 40. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 40 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 40, or a protein comprising a fragment of the amino acid sequence of SEQ ID 40 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID 40.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 41 from nucleotide 1575 to nucleotide 3038; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 41 from nucleotide 1650 to nucleotide 3038; (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vg3_1 deposited with the ATCC under accession number PTA-362; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone vg3_1 deposited with the ATCC under accession number PTA-362; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 42; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 42 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 42; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID NO: 41.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 41 from nucleotide 1575 to nucleotide 3038; the nucleotide sequence of SEQ ID 41 from nucleotide 1650 to nucleotide 3038; the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone

deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 42, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 42 having biological activity, the fragment comprising the amino acid sequence from amino acid 239 to amino acid 248 of SEQ ID 42.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 41.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (aa) SEQ ID but excluding the poly (A) tail at the 3'end of SEQ ID and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA-362; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID but excluding the poly (A) tail at the 3'end of SEQ ID and (bb) the nucleotide sequence of the insert of clone vg3_1 deposited with the ATCC under accession number PTA-362; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 41, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 41 to a nucleotide sequence corresponding to the 3'end of SEQ ID 41, but excluding the poly (A) tail at the 3'end of SEQ ID 41. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 41 from nucleotide 1575 to nucleotide 3038, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 41 from nucleotide 1575 to nucleotide to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 41 from nucleotide 1575 to nucleotide 3038. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 41 from nucleotide 1650 to nucleotide 3038, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 41 from nucleotide 1650 to nucleotide 3038, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 41 from nucleotide 1650 to nucleotide 3038.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 42; (b) a fragment of the amino acid sequence of SEQ ID 42, the fragment comprising eight contiguous amino acids of SEQ ID 42; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 42. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 42, or a protein comprising a fragment of the amino acid sequence of SEQ ID 42 having biological activity, the fragment comprising the amino acid sequence from amino acid 239 to amino acid 248 of SEQ ID 42.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 43; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 43 from nucleotide 2112 to nucleotide (c) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (d) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362; a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 44; (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 44 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 44; (i) a polynucleotide which is an allelic variant of a polynucleotide of above; a polynucleotide which encodes a species homologue of the protein of (g) or (h) above; (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in and (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in and that has a length that is at least 25% of the length of SEQ ID 43.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 43 from nucleotide 2112 to nucleotide 2363; the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 44, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 44 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID 44.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 43.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID 43, but excluding the poly (A) tail at the 3'end of SEQ ID 43; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA-362; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID 43, but excluding the poly (A) tail at the 3'end of SEQ ID 43; and (bb) the nucleotide sequence of the insert of clone vo2_ 1 deposited with the ATCC under accession number PTA-362; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 43, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 43 to a nucleotide sequence corresponding to the 3'end of SEQ ID 43, but excluding the poly (A) tail at the 3'end of SEQ ID 43. Also preferably the polynucleotide

isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 43 from nucleotide 2112 to nucleotide 2363, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 43 from nucleotide 2112 to nucleotide 2363, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 43 from nucleotide 2112 to nucleotide 2363.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 44; (b) a fragment of the amino acid sequence of SEQ ID 44, the fragment comprising eight contiguous amino acids of SEQ ID 44; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 44. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 44, or a protein comprising a fragment of the amino acid sequence of SEQ ID 44 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID 44.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 45; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 45 from nucleotide 36 to nucleotide 707; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 45 from nucleotide 393 to nucleotide 707; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 46; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 46 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 46; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least of the length of SEQ ID 45.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 45 from nucleotide 36 to nucleotide 707; the nucleotide sequence of SEQ ID 45 from nucleotide 393 to nucleotide 707; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA- 362; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 46, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 46 having biological activity, the fragment comprising the amino acid sequence. from amino acid 107 to amino acid 116 of SEQ ID 46.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 45.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID 45, but excluding the poly (A) tail at the 3'end of SEQ ID 45; and (ab) the nucleotide sequence of the insert of clone vo3_ 1 deposited with the ATCC under accession number PTA-362; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID 45, but excluding the poly (A) tail at the 3'end of SEQ ID 45; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA-362; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 45, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 45 to a nucleotide sequence corresponding to the 3'end of SEQ ID 45, but excluding the poly (A) tail at the 3'end of SEQ ID 45. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 45 from nucleotide 36 to nucleotide 707, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 45 from nucleotide 36 to nucleotide 707, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 45 from nucleotide 36 to nucleotide 707. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 45 from nucleotide 393 to nucleotide 707, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 45 from nucleotide 393 to nucleotide 707, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 45 from nucleotide 393 to nucleotide 707.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 46; fragment comprising eight contiguous amino acids of SEQ ID 46; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 46. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 46, or a protein comprising a fragment of the amino acid sequence of SEQ ID 46 having biological activity, the fragment comprising the amino acid sequence from amino acid 107 to amino acid 116 of SEQ ID 46.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting NO: 47; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 47 from nucleotide 74 to nucleotide 295; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (g) a polynucleotide encoding a mature protein encoded by the insert of clone

deposited with the ATCC under accession number PTA-362; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 48; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 48 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 48; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID NO: 47.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 47 from nucleotide 74 to nucleotide 295; the nucleotide sequence of SEQ ID 47 from nucleotide 134 to nucleotide 295; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA- 362; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by 362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 48, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 48 having biological activity, the fragment comprising the amino acid sequence from amino acid 32 to amino acid 41 of SEQ ID 48.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 47.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID 47, but excluding the poly (A) tail at the 3'end of SEQ ID 47; and (ab) the nucleotide sequence of the insert of clone (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (ba) SEQ ID NO: 47, but excluding the poly (A) tail at the 3'end of SEQ ID 47; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA-362; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 47, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 47 to a nucleotide sequence corresponding to the 3'end of SEQ ID 47, but excluding the poly (A) tail at the 3'end of SEQ ID 47. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 47 from nucleotide 74 to nucleotide 295, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 47 from nucleotide 74 to nucleotide 295, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 47 from nucleotide 74 to nucleotide 295. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 47 from nucleotide 134 to nucleotide 295, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 47 from nucleotide 134 to nucleotide 295, to a nucleotide sequence

corresponding to the 3'end of said sequence of SEQ ID 47 from nucleotide 134 to nucleotide 295.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 48; (b) a fragment of the amino acid sequence of SEQ ID 48, the fragment comprising eight contiguous amino acids of SEQ ID 48; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 48. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 48, or a protein comprising a fragment of the amino acid sequence of SEQ ID 48 having biological activity, the fragment comprising the amino acid sequence from amino acid 32 to amino acid 41 of SEQ ID 48.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 49; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 49 from nucleotide 45 to nucleotide 383; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 49 from nucleotide 312 to nucleotide 383; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 50; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 50 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 50; (j) a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in and that has a length that is at least of the length of SEQ ID NO: 49.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 49 from nucleotide 45 to nucleotide 383; the nucleotide sequence of SEQ ID 49 from nucleotide 312 to nucleotide 383; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA- 362; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 50 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 50, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 50 having biological activity, the fragment comprising the amino acid sequence from amino acid 51 to amino acid 60 of SEQ ID 50.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 49.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more

polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID 49, but excluding the poly (A) tail at the 3'end of SEQ ID 49; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA-362; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe(s); and (b) a process comprising the steps (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID 49, but excluding the poly (A) tail at the 3'end of SEQ ID 49; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA-362; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 49, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 49 to a nucleotide sequence corresponding to the 3'end of SEQ ID 49, but excluding the poly (A) tail at the 3'end of SEQ ID 49. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 49 from nucleotide 45 to nucleotide and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 49 from nucleotide 45 to nucleotide 383, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 49 from nucleotide 45 to nucleotide 383. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 49 from nucleotide 312 to nucleotide 383, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 49 from nucleotide 312 to nucleotide to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 49 from nucleotide 312 to nucleotide 383.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 50; (b) a fragment of the amino acid sequence of SEQ ID 50, the fragment comprising eight contiguous amino acids of SEQ ID 50; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 50. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 50 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 50, or a protein comprising a fragment of the amino acid sequence of SEQ ID 50 having biological activity, the fragment comprising the amino acid sequence from amino acid 51 to amino acid 60 of SEQ ID 50.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 51 from nucleotide 186 to nucleotide 1739; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 51 from nucleotide 288 to nucleotide 1739; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (e) a polynucleotide encoding the full-length protein encoded by the PTA-362; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 52; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 52 having biological activity, the

fragment comprising eight contiguous amino acids of SEQ ID 52; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least of the length of SEQ ID NO:

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 51 from nucleotide 186 to nucleotide 1739; the nucleotide sequence of SEQ ID 51 from nucleotide 288 to nucleotide 1739; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA- 362; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 52 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 52, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 52 having biological activity, the fragment comprising the amino acid sequence from amino acid 254 to amino acid 263 of SEQ ID 52.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO:

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID but excluding the poly (A) tail at the 3'end of SEQ ID and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA-362; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID but excluding the poly (A) tail at the 3'end of SEQ ID and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA-362; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 51, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 51 to a nucleotide sequence corresponding to the 3'end of SEQ ID 51, but excluding the poly (A) tail at the 3'end of SEQ ID 51. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 51 from nucleotide 186 to nucleotide 1739, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 51 from nucleotide 186 to nucleotide 1739, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 51 from nucleotide 186 to nucleotide 1739. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 51 from nucleotide 288 to nucleotide 1739, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 51 from nucleotide 288 to nucleotide 1739, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 51 from nucleotide 288 to nucleotide 1739.

In other embodiments, the present invention provides a composition comprising a protein, wherein said

protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 52; (b) a fragment of the amino acid sequence of SEQ ID 52, the fragment comprising eight contiguous amino acids of SEQ ID 52; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 52. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 52 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 52, or a protein comprising a fragment of the amino acid sequence of SEQ ID 52 having biological activity, the fragment comprising the amino acid sequence from amino acid 254 to amino acid 263 of SEQ ID 52.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 53; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 53 from nucleotide 440 to nucleotide 835; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 53 from nucleotide 632 to nucleotide 835; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone vol deposited with the ATCC under accession number PTA-366; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone vol deposited with the ATCC under accession number PTA-366; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (g) a polynucleotide encoding a mature protein encoded by the insert of clone vol deposited with the ATCC under accession number PTA- 366; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 54; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 54 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 54; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID 53.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 53 from nucleotide 440 to nucleotide 835; the nucleotide sequence of SEQ ID 53 from nucleotide 632 to nucleotide 835; the nucleotide sequence of the full-length protein coding sequence of clone vo deposited with the ATCC under accession number PTA- or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone vol with the ATCC under accession number PTA- 366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 54, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 54 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID 54.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 53.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (aa) SEQ ID but excluding the poly (A) tail at the 3'end of SEQ ID 53; and (ab) the nucleotide sequence of the insert of clone vol deposited with the ATCC under (ii) hybridizing said probe

(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (ba) SEQ ID NO: 53, but excluding the poly (A) tail at the 3'end of SEQ ID 53; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 366; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 53, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 53 to a nucleotide sequence corresponding to the 3'end of SEQ ID 53, but excluding the poly (A) tail at the 3'end of SEQ ID 53. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 53 from nucleotide 440 to nucleotide 835, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 53 from nucleotide 440 to nucleotide 835, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 53 from nucleotide 440 to nucleotide 835. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 53 from nucleotide 632 to nucleotide 835, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 53 from nucleotide 632 to nucleotide 835.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 54; (b) a fragment of the amino acid sequence of SEQ ID 54, the fragment comprising eight contiguous amino acids of SEQ ID 54; and (c) the amino acid sequence encoded by the insert of clone vol 1_1 deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 54. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 54, or a protein comprising a fragment of the amino acid sequence of SEQ ID 54 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID 54.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 55; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 55 from nucleotide 72 to nucleotide 329; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 55 from nucleotide 120 to nucleotide 329; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 366; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 56; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 56 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 56; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a

polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID NO: 55.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 55 from nucleotide 72 to nucleotide 329; the nucleotide sequence of SEQ ID 55 from nucleotide 120 to nucleotide 329; the nucleotide sequence of the full-length protein coding sequence of clone vo deposited with the ATCC under accession number PTA- 366; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 56, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 56 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID 56.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 55.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID but excluding the poly (A) tail at the 3'end of SEQ ID 55; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA-366; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID 55, but excluding the poly (A) tail at the 3'end of SEQ ID 55; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA-366; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 55, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 55 to a nucleotide sequence corresponding to the 3'end of SEQ ID 55, but excluding the poly (A) tail at the 3'end of SEQ ID 55. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 55 from nucleotide 72 to nucleotide 329, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 55 from nucleotide 72 to nucleotide 329, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 55 from nucleotide 72 to nucleotide 329. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 55 from nucleotide 120 to nucleotide 329, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 55 from nucleotide 120 to nucleotide 329, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 55 from nucleotide 120 to nucleotide 329.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 56; (b) a fragment of the amino acid sequence of SEQ ID 56, the fragment

comprising eight contiguous amino acids of SEQ ID 56; and the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 56. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 56, or a protein comprising a fragment of the amino acid sequence of SEQ ID 56 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID 56.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 57; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 57 from nucleotide 227 to nucleotide 439; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 57 from nucleotide 287 to nucleotide 439; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 366; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 58; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 58 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 58; (j) a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID NO: 57.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 57 from nucleotide 227 to nucleotide 439; the nucleotide sequence of SEQ ID 57 from nucleotide 287 to nucleotide 439; the nucleotide sequence of the full-length protein coding sequence of clone vo 13_1 deposited with the ATCC under accession number PTA- 366; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 58 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 58, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 58 having biological activity, the fragment comprising the amino acid sequence from amino acid 30 to amino acid 39 of SEQ ID 58.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 57.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID 57, but excluding the poly (A) tail at the 3'end of SEQ ID 57; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 366; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as

4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID 57, but excluding the poly (A) tail at the 3'end of SEQ ID 57; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 366; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 57, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 57 to a nucleotide sequence corresponding to the 3'end of SEQ ID 57, but excluding the poly (A) tail at the 3'end of SEQ ID 57. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 57 from nucleotide 227 to nucleotide 439, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 57 from nucleotide 227 to nucleotide 439, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 57 from nucleotide 227 to nucleotide 439. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 57 from nucleotide 287 to nucleotide 439, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 57 from nucleotide 287 to nucleotide 439, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 57 from nucleotide 287 to nucleotide 439.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 58; (b) a fragment of the amino acid sequence of SEQ ID 58, the fragment comprising eight contiguous amino acids of SEQ ID 58; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 58. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 58 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 58, or a protein comprising a fragment of the amino acid sequence of SEQ ID 58 having biological activity, the fragment comprising the amino acid sequence from amino acid 30 to amino acid 39 of SEQ ID 58.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 59; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 59 from nucleotide 96 to nucleotide 341; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 59 from nucleotide 174 to nucleotide 341; (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 366; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 60; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 60 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 60; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in

(a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID NO: 59.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 59 from nucleotide 96 to nucleotide 341; the nucleotide sequence of SEQ ID 59 from nucleotide 174 to nucleotide the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA- 366; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 60 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 60, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 60 having biological activity, the fragment comprising the amino acid sequence from amino acid 36 to amino acid 45 of SEQ ID 60.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 59.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (aa) SEQ ID but excluding the poly (A) tail at the 3'end of SEQ ID 59; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 366; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID 59, but excluding the poly (A) tail at the 3'end of SEQ ID 59; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 366; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 59, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 59 to a nucleotide sequence corresponding to the 3'end of SEQ ID 59, but excluding the poly (A) tail at the 3'end of SEQ ID 59. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 59 from nucleotide 96 to nucleotide and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 59 from nucleotide 96 to nucleotide to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 59 from nucleotide 96 to nucleotide 341. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 59 from nucleotide 174 to nucleotide 341, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 59 from nucleotide 174 to nucleotide to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 59 from nucleotide 174 to nucleotide 341.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 60; (b) a fragment of the amino acid sequence of SEQ ID 60, the fragment comprising eight contiguous amino acids of SEQ ID 60; and (c) the amino acid sequence encoded by the

insert of clone deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 60. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 60 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 60, or a protein comprising a fragment of the amino acid sequence of SEQ ID 60 having biological activity, the fragment comprising the amino acid sequence from amino acid 36 to amino acid 45 of SEQ ID 60.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 61; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 61 from nucleotide 90 to nucleotide 599; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 61 from nucleotide 165 to nucleotide 599; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 366; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 62; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 62 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 62; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID NO: 61.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 61 from nucleotide 90 to nucleotide 599; the nucleotide sequence of SEQ ID 61 from nucleotide 165 to nucleotide 599; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA- 366; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 62, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 62 having biological activity, the fragment comprising the amino acid sequence from amino acid 80 to amino acid 89 of SEQ ID 62.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 61.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID 61, but excluding the poly (A) tail 3'end of SEQ ID and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 366; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process

comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID NO: but excluding the poly (A) tail at the 3'end of SEQ ID and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 366; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 61, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 61 to a nucleotide sequence corresponding to the 3'end of SEQ ID 61, but excluding the poly (A) tail at the 3'end of SEQ ID 61. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 61 from nucleotide 90 to nucleotide 599, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 61 from nucleotide 90 to nucleotide 599, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 61 from nucleotide 90 to nucleotide 599. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID NO: 61 from nucleotide 165 to nucleotide 599, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 61 from nucleotide 165 to nucleotide 599, to nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 61 from nucleotide 165 to nucleotide 599.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 62; (b) a fragment of the amino acid sequence of SEQ ID 62, the fragment comprising eight contiguous amino acids of SEQ ID 62; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 62. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 62, or a protein comprising a fragment of the amino acid sequence of SEQ ID 62 having biological activity, the fragment comprising the amino acid sequence from amino acid 80 to amino acid 89 of SEQ ID 62.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 63; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 63 from nucleotide 209 to nucleotide (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 63 from nucleotide 398 to nucleotide (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 366; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 64; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 64 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 64; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the

polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID 63.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 63 from nucleotide 209 to nucleotide the nucleotide sequence of SEQ ID 63 from nucleotide 398 to nucleotide the nucleotide sequence of the full-length protein coding sequence of clone vo 16_1 deposited with the ATCC under accession number PTA- 366; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 64 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 64, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 64 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID 64.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 63.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (aa) SEQ ID 63, but excluding the poly (A) tail at the 3'end of SEQ ID 63; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA-366; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID NO: 63, but excluding the poly (A) tail at the 3'end of SEQ ID 63; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 366; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 63, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 63 to a nucleotide sequence corresponding to the 3'end of SEQ ID 63, but excluding the poly (A) tail at the 3'end of SEQ ID 63. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 63 from nucleotide 209 to nucleotide and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 63 from nucleotide 209 to nucleotide to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 63 from nucleotide 209 to nucleotide Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 63 from nucleotide 398 to nucleotide 451, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 63 from nucleotide to nucleotide to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 63 from nucleotide 398 to nucleotide 451.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 64; (b) a fragment of the amino acid sequence of SEQ ID 64, the fragment comprising eight contiguous amino acids of SEQ ID 64; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid

sequence of SEQ ID 64. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 64 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 64, or a protein comprising a fragment of the amino acid sequence of SEQ ID 64 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID 64.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 65; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 65 from nucleotide 31 to nucleotide (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 65 from nucleotide 97 to nucleotide (d) a polynucleotide comprising the nucleotide sequence of the full- accession number PTA-366; (e) a polynucleotide encoding the full-length protein encoded by the PTA-366; a polynucleotide comprising the nucleotide sequence of a mature accession number PTA-366; (g) a polynucleotide encoding a mature protein encoded by the insert of clone vol8_1 deposited with the ATCC under accession number PTA-366; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 66; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 66 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 66; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in that has a length that is at least 25% of the length of SEQ ID NO: 65.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 65 from nucleotide 31 to nucleotide the nucleotide sequence of SEQ ID 65 from nucleotide 97 to nucleotide the nucleotide sequence of the full-length protein coding sequence of clone vo 18_1 deposited with the ATCC under accession number PTA- 366; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone vo 18_ 1 deposited with the ATCC under accession number PTA- 366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 66 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 66, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 66 having biological activity, the fragment comprising the amino acid sequence from amino acid 28 to amino acid 37 of SEQ ID 66.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 65.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID 65, but excluding the poly (A) tail at the 3'end of SEQ ID 65; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 366; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (ba) SEQ ID 65, but excluding the poly (A) tail at the 3'end of SEQ ID 65; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 366; (ii) hybridizing said primer (s) to

human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID excluding the poly (A) tail at the 3'end of SEQ ID 65. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 65 from nucleotide 31 to nucleotide and extending contiguously from a nucleotide sequence corresponding to the 5'end sequence corresponding to the 3'end of said sequence of SEQ ID 65 from nucleotide 31 to nucleotide Also preferably the polynucleotide isolated according to the above nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 65 from nucleotide 97 to nucleotide to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 65 from nucleotide 97 to nucleotide

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins. Preferably such embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 66 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 66, or a protein comprising a fragment of the amino acid sequence of SEQ ID 66 having biological activity, the fragment comprising the amino acid sequence

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 67; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 67 from nucleotide 23 to nucleotide 736; a polynucleotide comprising the nucleotide sequence of SEQ ID 67 from nucleotide 83 to nucleotide 736; (d) a polynucleotide comprising the nucleotide sequence of the full- accession number PTA-366; (e) a polynucleotide encoding the full-length protein encoded by the PTA-366; a polynucleotide comprising the nucleotide sequence of a mature accession number PTA-366; (g) a polynucleotide encoding a mature protein encoded by the 366; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 68; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 68 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 68; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in and that has a length that is at least 25% of the length of SEQ ID NO: 67.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 67 from nucleotide 23 to nucleotide 736; the nucleotide sequence of SEQ ID 67 from nucleotide 83 to nucleotide 736; the nucleotide sequence of the full-length protein coding sequence of clone vo 19_ 1 deposited with the ATCC under accession number PTA- 366; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 68 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 68, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 68 having biological

activity, the fragment comprising the amino acid sequence from amino acid 114 to amino acid 123 of SEQ ID 68.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 67.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID 67, but excluding the poly (A) tail at the 3'end of SEQ ID 67; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 366; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID 67, but excluding the poly (A) tail at the 3'end of SEQ ID 67; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 366; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 67, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 67 to a nucleotide sequence corresponding to the 3'end of SEQ ID 67, but excluding the poly (A) tail at the 3'end of SEQ ID 67. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 67 from nucleotide 23 to nucleotide 736, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 67 from nucleotide 23 to nucleotide 736, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 67 from nucleotide 23 to nucleotide 736. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 67 from nucleotide 83 to nucleotide 736, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 67 from nucleotide 83 to nucleotide 736, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 67 from nucleotide 83 to nucleotide 736 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 68; (b) a fragment of the amino acid sequence of SEQ ID 68, the fragment comprising eight contiguous amino acids of SEQ ID 68; and (c) the amino acid sequence encoded by the insert of clone vol9_1 deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 68. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 68 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 68, or a protein comprising a fragment of the amino acid sequence of SEQ ID 68 having biological activity, the fragment comprising the amino acid sequence from amino acid 114 to amino acid 123 of SEQ ID 68.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 69; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 69 from nucleotide 104 to nucleotide 1399; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 69 from nucleotide 158 to nucleotide 1399; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC

under accession number PTA-366; accession number PTA-366; (g) a polynucleotide encoding a mature protein encoded by the 366; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 70; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 70 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 70; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID NO: 69.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 69 from nucleotide 104 to nucleotide 1399; the nucleotide sequence of SEQ ID 69 from nucleotide 158 to nucleotide 1399; the nucleotide sequence of the full-length protein deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by 366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 70 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 70, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 70 having biological activity, the fragment comprising the amino acid sequence from amino acid 211 to amino acid 220 of SEQ ID 70.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 69.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID 69, but excluding the poly (A) tail at the 3'end of SEQ ID 69; and (ab) the nucleotide sequence of the insert of clone 366; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID 69, but excluding the poly (A) tail at the 3'end of SEQ ID 69; and (bb) the nucleotide sequence of the insert of clone 366; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 69, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 69 to a nucleotide sequence corresponding to the 3'end of SEQ ID 69, but excluding the poly (A) tail at the 3'end of SEQ ID 69. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 69 from nucleotide 104 to nucleotide 1399, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 69 from nucleotide 104 to nucleotide 1399, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 69 from nucleotide 104 to nucleotide 1399. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 69 from nucleotide 158 to nucleotide 1399, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 69 from nucleotide 158 to nucleotide 1399, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 69 from nucleotide 158 to nucleotide 1399.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 70; (b) a fragment of the amino acid sequence of SEQ ID 70, the fragment comprising eight contiguous amino acids of SEQ ID 70; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 70. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 70 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 70, or a protein comprising a fragment of the amino acid sequence of SEQ ID 70 having biological activity, the fragment comprising the amino acid sequence from amino acid 211 to amino acid 220 of SEQ ID 70.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 71; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 71 from nucleotide 174 to nucleotide 1595; (c) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (d) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366; a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 366; (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 72; (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 72 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 72; (i) a polynucleotide which is an allelic variant of a polynucleotide of above; a polynucleotide which encodes a species homologue of the protein of (g) or (h) above; (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in and (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in and that has a length that is at least of the length of SEQ ID

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 71 nucleotide 1595; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 72 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 72, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 72 having biological activity, the fragment comprising the amino acid sequence from amino acid 232 to amino acid 241 of SEQ ID 72.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO:

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (aa) SEQ ID but excluding the poly (A) tail at the 3'end of SEQ ID and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 366; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at

50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (ba) SEQ ID but excluding the poly (A) tail at the 3'end of SEQ ID and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 366; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 71, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 71 to a nucleotide sequence corresponding to the 3'end of SEQ ID 71, but excluding the poly (A) tail at the 3'end of SEQ ID Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 71 from nucleotide 174 to nucleotide 1595, and extending contiguously from a nucleotide sequence corresponding to the 5'end 71 from nucleotide 174 to nucleotide 1595, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 71 from nucleotide 174 to nucleotide 1595.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 72; (b) a fragment of the amino acid sequence of SEQ ID 72, the fragment comprising eight contiguous amino acids of SEQ ID 72; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 72. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 72 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 72, or a protein comprising a fragment of the amino acid sequence of SEQ ID 72 having biological activity, the fragment comprising the amino acid sequence from amino acid 232 to amino acid 241 of SEQ ID 72.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 73; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 73 from nucleotide 129 to nucleotide 311; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 73 from nucleotide 195 to nucleotide 311; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 366; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 74; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 74 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 74; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least of the length of SEQ ID 73.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 73 from nucleotide 129 to nucleotide 311; the nucleotide sequence of SEQ ID 73 from nucleotide 195 to nucleotide 311; the

nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA- 366; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 74 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 74, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 74 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID 74.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 73.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID 73, but excluding the poly (A) tail at the 3'end of SEQ ID 73; and the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA-366; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID 73, but excluding the poly (A) tail at the 3'end of SEQ ID 73; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 366; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 73, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID excluding the poly (A) tail at the 3'end of SEQ ID NO: 73. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 73 from nucleotide 129 to nucleotide 311, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 73 from nucleotide 129 to nucleotide 311, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 73 from nucleotide 129 to nucleotide 311. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 73 from nucleotide 195 to nucleotide 311, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 73 from nucleotide 195 to nucleotide 311, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 73 from nucleotide 195 to nucleotide 311.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 74; (b) a fragment of the amino acid sequence of SEQ ID 74, the fragment comprising eight contiguous amino acids of SEQ ID 74; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 74. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 74 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 74, or a protein comprising a fragment of the amino acid sequence of SEQ ID 74

having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID 74.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 75; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 75 from nucleotide 73 to nucleotide 798; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 75 from nucleotide 142 to nucleotide 798; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 366; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 76; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 76 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 76; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID 75.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 75 from nucleotide 73 to nucleotide 798; the nucleotide sequence of SEQ ID 75 from nucleotide 142 to nucleotide 798; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA- 366; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 76 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 76, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 76 having biological activity, the fragment comprising the amino acid sequence from amino acid 116 to amino acid 125 of SEQ ID 76.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 75.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID 75, but excluding the poly (A) tail at the 3'end of SEQ ID 75; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 366; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID 75, but excluding the poly (A) tail at the 3'end of SEQ ID 75; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 366; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 75, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 75 to a nucleotide sequence corresponding to the 3'end of SEQ ID 75, but excluding the poly (A) tail at the 3'end of SEQ ID 75. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 75 from nucleotide 73 to nucleotide 798, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 75 from nucleotide 73 to nucleotide 798, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 75 from nucleotide 73 to nucleotide 798. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 75 from nucleotide 142 to nucleotide 798, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 75 from nucleotide 142 to nucleotide 798, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 75 from nucleotide 142 to nucleotide 798.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 76; (b) a fragment of the amino acid sequence of SEQ ID 76, the fragment comprising eight contiguous amino acids of SEQ ID 76; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 76. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 76 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 76, or a protein comprising a fragment of the amino acid sequence of SEQ ID 76 having biological activity, the fragment comprising the amino acid sequence from amino acid 116 to amino acid 125 of SEQ ID 76.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 77; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 77 from nucleotide 26 to nucleotide 307; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 77 from nucleotide 101 to nucleotide 307; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 366; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 78; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 78 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 78; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID NO: 77.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 77 from nucleotide 26 to nucleotide 307; the nucleotide sequence of SEQ ID 77 from nucleotide to nucleotide 307; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA- 366; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide

encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 78, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 78 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID 78.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 77.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (aa) SEQ ID 77, but excluding the poly (A) tail at the 3'end of SEQ ID 77; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA-366; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID 77, but excluding the poly (A) tail at the 3'end of SEQ ID 77; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 366; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 77, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 77 to a nucleotide sequence corresponding to the 3'end of SEQ ID 77, but excluding the poly (A) tail at the 3'end of SEQ ID 77. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 77 from nucleotide 26 to nucleotide 307, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 77 from nucleotide 26 to nucleotide 307, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 77 from nucleotide 26 to nucleotide 307. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 77 from nucleotide 101 to nucleotide 307, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 77 from nucleotide 101 to nucleotide 307, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 77 from nucleotide 101 to nucleotide 307.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 78; (b) a fragment of the amino acid sequence of SEQ ID 78, the fragment comprising eight contiguous amino acids of SEQ ID 78; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 78. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 78, or a protein comprising a fragment of the amino acid sequence of SEQ ID 78 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID 78.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 79; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 79 from nucleotide 43 to nucleotide 228; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 79 from nucleotide 94 to nucleotide 228; (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp23_1 deposited with the ATCC under accession number PTA-368; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp23_1 deposited with the ATCC under accession number PTA-368; (g) a polynucleotide encoding a mature protein encoded by the insert of clone vp23_1 deposited with the ATCC under accession number PTA- 368; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 80; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 80 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 80; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID NO: 79.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO: 79 from nucleotide 43 to nucleotide 228; the nucleotide sequence of SEQ ID 79 from nucleotide 94 to nucleotide 228; the nucleotide sequence of the full-length protein coding sequence of clone vp23_1 deposited with the ATCC under accession number PTA- 368; or the nucleotide sequence of a mature protein coding sequence of clone vp23_1 deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone vp23_1 deposited with the ATCC under accession number PTA- 368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 80, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 80 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID 80.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 79.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID 79, but excluding the poly (A) tail at the 3'end of SEQ ID 79; and (ab) the nucleotide sequence of the insert of clone ATCC under accession (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID NO: 79, but excluding the poly (A) tail at the 3'end of SEQ ID 79; and (bb) the nucleotide sequence of the insert of clone vp23_1 deposited with the ATCC under accession number PTA- 368; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

corresponding to the sequence of SEQ ID 79, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 79 to a nucleotide sequence corresponding to the 3'end of SEQ ID 79, but excluding the poly (A) tail at the 3'end of SEQ ID 79. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 79 from nucleotide 43 to nucleotide 228, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 79 from nucleotide 43 to nucleotide 228, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 79 from nucleotide 43 to nucleotide 228. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 79 from nucleotide 94 to nucleotide 228, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 79 from nucleotide 94 to nucleotide 228.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 80; (b) a fragment of the amino acid sequence of SEQ ID 80, the fragment comprising eight contiguous amino acids of SEQ ID 80; and (c) the amino acid sequence encoded by the insert of clone vp23_1 deposited with the ATCC under accession number PTA-368; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 80. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 80, or a protein comprising a fragment of the amino acid sequence of SEQ ID 80 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID 80.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 81 from nucleotide 245 to nucleotide 427; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 81 from nucleotide 308 to nucleotide 427; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 82; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 82 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 82; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID NO: 81.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 81 from nucleotide 245 to nucleotide 427; the nucleotide sequence of SEQ ID 81 from nucleotide 308 to nucleotide 427; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA- 368; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the

polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 82 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 82, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 82 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID 82.

Other embodiments provide the gene corresponding to the sequence of SEQ 81.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (aa) SEQ ID but excluding the poly (A) tail at the 3'end of SEQ ID and (ab) the nucleotide sequence of the insert of clone vq7_1 deposited with the ATCC under accession number PTA-368; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (ba) SEQ ID but excluding the poly (A) tail at the 3'end of SEQ ID and (bb) the nucleotide sequence of the insert of clone vq7_1 deposited with the ATCC under accession number PTA-368; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 81, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID excluding the poly (A) tail at the 3'end of SEQ ID 81. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 81 from nucleotide 245 to nucleotide 427, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 81 from nucleotide 245 to nucleotide 427, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 81 from nucleotide 245 to nucleotide 427. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 81 from nucleotide 308 to nucleotide 427, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 81 from nucleotide 308 to nucleotide 427, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 81 from nucleotide 308 to nucleotide 427.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 82; (b) a fragment of the amino acid sequence of SEQ ID 82, the fragment comprising eight contiguous amino acids of SEQ ID 82; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-368; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 82. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 82 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 82, or a protein comprising a fragment of the amino acid sequence of SEQ ID 82 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID 82.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 83; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 83 from nucleotide 119 to nucleotide 475; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 83 from nucleotide 185 to nucleotide 475; (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (g) a polynucleotide encoding a mature protein encoded by the insert of clone vq8_1 deposited with the ATCC under accession number PTA-368; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 84; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 84 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 84; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID 83.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 83 from nucleotide 119 to nucleotide 475; the nucleotide sequence of SEQ ID 83 from nucleotide 185 to nucleotide 475; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA- 368; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 84 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 84, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 84 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID 84.

Other embodiments provide the gene corresponding to the sequence of SEQ ID 83.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID but excluding the poly (A) tail at the 3'end of SEQ ID 83; and (ab) the nucleotide sequence of the insert of clone vq8_1 deposited with the ATCC under accession number PTA-368; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID 83, but excluding the poly (A) tail at the 3'end of SEQ ID 83; and (bb) the nucleotide sequence of the insert of clone vq8_ 1 deposited with the ATCC under accession number PTA-368; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 83, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 83 to a nucleotide sequence corresponding to the 3'end of SEQ ID

83, but excluding the poly (A) tail at the 3'end of SEQ ID 83. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID NO: 83 from nucleotide 119 to nucleotide 475, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 83 from nucleotide 119 to nucleotide 475, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 83 from nucleotide 119 to nucleotide 475. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 83 from nucleotide 185 to nucleotide 475, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 83 from nucleotide 185 to nucleotide 475, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 83 from nucleotide 185 to nucleotide 475.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 84; (b) a fragment of the amino acid sequence of SEQ ID 84, the fragment comprising eight contiguous amino acids of SEQ ID 84; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-368; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 84. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 84 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 84, or a protein comprising a fragment of the amino acid sequence of SEQ ID 84 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID 84.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 85; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 85 from nucleotide 90 to nucleotide 323; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 85 from nucleotide 141 to nucleotide 323; (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq9_1 deposited with the ATCC under accession number PTA-368; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; protein coding sequence of clone vq9_1 deposited with the ATCC under accession number PTA-368; (g) a polynucleotide encoding a mature protein encoded by the insert of clone vq9_1 deposited with the (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 86; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 86 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 86; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID 85.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 85 from nucleotide 90 to nucleotide 323; the nucleotide sequence of SEQ ID 85 from nucleotide 141 to nucleotide 323; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA- 368; or the nucleotide sequence of a mature protein coding sequence of clone vq9_1 deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 86 having biological activity, the fragment preferably comprising eight (more preferably twenty,

most preferably thirty) contiguous amino acids of SEQ ID 86, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 86 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID 86.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 85.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID 85, but excluding the poly (A) tail at the 3'end of SEQ ID 85; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (ba) SEQ ID but excluding the poly (A) tail at the 3'end of SEQ ID 85; and (bb) the nucleotide sequence of the insert of clone vq9_1 deposited with the ATCC under accession number PTA-368; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii). Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 85, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID excluding the poly (A) tail at the 3'end of SEQ ID 85. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence 323, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 85 from nucleotide 90 to nucleotide 323, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 85 from nucleotide 90 to nucleotide 323. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 85 from nucleotide 141 to nucleotide 323, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 85 from nucleotide 141 to nucleotide 323, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 85 from nucleotide 141 to nucleotide 323.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 86; fragment comprising eight contiguous amino acids of SEQ ID 86; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-368; the protein being substantially free from other mammalian proteins. Preferably such embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 86 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID or a protein comprising a fragment of the amino acid sequence of SEQ ID 86 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID 86.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 87; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 87 from nucleotide 18 to nucleotide 452; a polynucleotide comprising the nucleotide sequence of SEQ ID 87 from nucleotide 72 to nucleotide 452; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone with the ATCC under accession number PTA-368; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; a polynucleotide comprising the nucleotide sequence of a mature protein

coding sequence of clone deposited with the ATCC under accession number PTA-368; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 368; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 88; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 88 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 88; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID NO: 87.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 87 from nucleotide 18 to nucleotide 452; the nucleotide sequence of SEQ ID 87 from nucleotide 72 to nucleotide 452; the nucleotide sequence of the full-length protein coding sequence of clone vq 10_ 1 deposited with the ATCC under accession number PTA- 368; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone deposited with the ATCC under accession number PTA- 368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 88 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 88, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 88 having biological activity, the fragment comprising the amino acid sequence from amino acid 67 to amino acid 76 of SEQ ID 88.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 87.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (aa) SEQ ID 87, but excluding the poly (A) tail at the 3'end of SEQ ID 87; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA-368; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID NO: 87, but excluding the poly (A) tail at the 3'end of SEQ ID 87; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 368; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 87, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 87 to a nucleotide sequence corresponding to the 3'end of SEQ ID 87, but excluding the poly (A) tail at the 3'end of SEQ ID 87. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 87 from nucleotide 18 to nucleotide 452, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 87 from nucleotide 18 to nucleotide 452, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 87 from nucleotide 18 to nucleotide 452. Also preferably the polynucleotide isolated according to the above process

comprises a nucleotide sequence corresponding to the sequence of SEQ ID 87 from nucleotide 72 to nucleotide 452, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 87 from nucleotide 72 to nucleotide 452, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 87 from nucleotide 72 to nucleotide 452.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 88; (b) a fragment of the amino acid sequence of SEQ ID 88, the fragment comprising eight contiguous amino acids of SEQ ID 88; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-368; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 88. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 88 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID or a protein comprising a fragment of the amino acid sequence of SEQ ID 88 having biological activity, the fragment comprising the amino acid sequence from amino acid 67 to amino acid 76 of SEQ ID 88.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 89; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 89 from nucleotide 196 to nucleotide 378; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 89 from nucleotide 262 to nucleotide 378; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 368; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 90; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 90 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 90; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID NO: 89.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 89 from nucleotide 196 to nucleotide 378; the nucleotide sequence of SEQ ID 89 from nucleotide 262 to nucleotide 378; the nucleotide sequence of the full-length protein coding sequence of clone vq deposited with the ATCC under accession number PTA- 368; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 90 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 90, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 90 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID 90.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 89.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID NO: 89, but excluding the poly (A) tail at the 3'end of SEQ ID 89; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 368; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID 89, but excluding the poly (A) tail at the 3'end of SEQ ID and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 368; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 89, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 89 to a nucleotide sequence corresponding to the 3'end of SEQ ID 89, but excluding the poly (A) tail at the 3'end of SEQ ID 89. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID from nucleotide 196 to nucleotide 378, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 89 from nucleotide 196 to nucleotide 378, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 89 from nucleotide 196 to nucleotide 378. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 89 from nucleotide 262 to nucleotide 378, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 89 from nucleotide 262 to nucleotide 378, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 89 from nucleotide 262 to nucleotide 378.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 90; (b) a fragment of the amino acid sequence of SEQ ID 90, the fragment comprising eight contiguous amino acids of SEQ ID 90; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-368; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 90. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 90 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 90, or a protein comprising a fragment of the amino acid sequence of SEQ ID 90 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID 90.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 91; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 91 from nucleotide 35 to nucleotide 718; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 91 from nucleotide 173 to nucleotide 718; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under

accession number PTA- 368; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 92; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 92 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 92; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least of the length of SEQ ID

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO: 91 from nucleotide 35 to nucleotide 718; the nucleotide sequence of SEQ ID 91 from nucleotide 173 to nucleotide 718; the nucleotide sequence of the full-length protein coding sequence of clone vq deposited with the ATCC under accession number PTA- 368; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 92 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 92, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 92 having biological activity, the fragment comprising the amino acid sequence from amino acid 109 to amino acid 118 of SEQ ID 92.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO:

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID NO: but excluding the poly (A) tail at the 3'end of SEQ ID and (ab) the nucleotide sequence of the insert of clone vq deposited with the ATCC under accession number (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of : (ba) SEQ ID but excluding the poly (A) tail at the 3'end of SEQ ID and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 368; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 91, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 91 to a nucleotide sequence corresponding to the 3'end of SEQ ID 91, but excluding the poly (A) tail at the 3'end of SEQ ID 91. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 91 from nucleotide 35 to nucleotide 718, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 91 from nucleotide 35 to nucleotide 718, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 91 from nucleotide 35 to nucleotide 718. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 91 from nucleotide 173 to nucleotide 718, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 91 from nucleotide 173 to nucleotide 718.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 92; (b) a fragment of the amino acid sequence of SEQ ID 92, the fragment comprising eight contiguous amino acids of SEQ ID 92; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-368; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 92. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 92 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 92, or a protein comprising a fragment of the amino acid sequence of SEQ ID 92 having biological activity, the fragment comprising the amino acid sequence from amino acid 109 to amino acid 118 of SEQ ID 92.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 93; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 93 from nucleotide 1 to nucleotide 762; a polynucleotide comprising the nucleotide sequence of SEQ ID 93 from nucleotide 70 to nucleotide 762; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 368; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 94; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 94 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 94; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least of the length of SEQ ID 93.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 93 from nucleotide 1 to nucleotide 762; the nucleotide sequence of SEQ ID 93 from nucleotide 70 to nucleotide 762; the nucleotide sequence of the full-length protein coding sequence of clone vq deposited with the ATCC under accession number PTA- 368; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone vq 19_ 1 deposited with the ATCC under accession number PTA- 368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 94, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 94 having biological activity, the fragment comprising the amino acid sequence from amino acid 122 to amino acid 131 of SEQ ID 94.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 93.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from

the group consisting of: (aa) SEQ ID 93, but excluding the poly (A) tail 3'end of SEQ ID 93; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA-368; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID 93, but excluding the poly (A) tail at the 3'end of SEQ ID 93; and (bb) the nucleotide sequence of the insert of clone vq deposited with the ATCC under accession number (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 93, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 93 to a nucleotide sequence corresponding to the 3'end of SEQ ID 93, but excluding the poly (A) tail at the 3'end of SEQ ID 93. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 93 from nucleotide 1 to nucleotide 762, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 93 from nucleotide 1 to nucleotide 762, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 93 from nucleotide 1 to nucleotide 762. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 93 from nucleotide 70 to nucleotide 762, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 93 from nucleotide 70 to nucleotide 762, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 93 from nucleotide 70 to nucleotide 762.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 94; (b) a fragment of the amino acid sequence of SEQ ID 94, the fragment comprising eight contiguous amino acids of SEQ ID 94; and the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-368; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 94. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 94, or a protein comprising a fragment of the amino acid sequence of SEQ ID 94 having biological activity, the fragment comprising the amino acid sequence from amino acid 122 to amino acid 131 of SEQ ID 94.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 95; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 95 from nucleotide 106 to nucleotide 792; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 95 from nucleotide 172 to nucleotide 792; (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone vq20_1 deposited with the ATCC under accession number PTA-368; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (g) a polynucleotide encoding a mature protein encoded by the insert of clone vq20_1 deposited with the ATCC under accession number PTA- 368; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 96; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 96 having biological activity, the fragment comprising eight

contiguous amino acids of SEQ ID 96; (j) a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID NO: 95.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 95 from nucleotide 106 to nucleotide 792; the nucleotide sequence of SEQ ID 95 from nucleotide 172 to nucleotide 792; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA- 368; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 96 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 96, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 96 having biological activity, the fragment comprising the amino acid sequence from amino acid 109 to amino acid 118 of SEQ ID 96.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 95.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID 95, but excluding the poly (A) tail at the 3'end of SEQ ID 95; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 368; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe(s); and (b) a process comprising the steps of: preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID NO: 95, but excluding the poly (A) tail at the 3'end of SEQ ID 95; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 368; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 95, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 95 to a nucleotide sequence corresponding to the 3'end of SEQ ID 95, but excluding the poly (A) tail at the 3'end of SEQ ID 95. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 95 from nucleotide 106 to nucleotide 792, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 95 from nucleotide 106 to nucleotide 792, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 95 from nucleotide 106 to nucleotide 792. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 95 from nucleotide 172 to nucleotide 792, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 95 from nucleotide 172 to nucleotide 792, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 95 from nucleotide 172 to nucleotide 792.

In other embodiments, the present invention provides a composition comprising a protein, wherein said

protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 96; (b) a fragment of the amino acid sequence of SEQ ID 96, the fragment comprising eight contiguous amino acids of SEQ ID 96; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-368; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 96. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 96 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 96, or a protein comprising a fragment of the amino acid sequence of SEQ ID 96 having biological activity, the fragment comprising the amino acid sequence from amino acid 109 to amino acid 118 of SEQ ID 96.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 97; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 97 from nucleotide 40 to nucleotide 315; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 97 from nucleotide 124 to nucleotide 315; (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 368; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 98; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 98 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 98; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID NO: 97.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 97 from nucleotide 40 to nucleotide 315; the nucleotide sequence of SEQ ID 97 from nucleotide 124 to nucleotide 315; the nucleotide sequence of the full-length protein coding sequence of clone vq21_1 deposited with the ATCC under accession number PTA- 368; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone vq21_1 deposited with the ATCC under accession number PTA- 368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 98 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 98, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 98 having biological activity, the fragment comprising the amino acid sequence from amino acid 41 to amino acid 50 of SEQ ID 98.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 97.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from

the group consisting (aa) SEQ ID 97, but excluding the poly (A) tail at the 3'end of SEQ ID 97; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA-368; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe(s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID 97, but excluding the poly (A) tail at the 3'end of SEQ ID 97; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 368; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 97, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 97 to a nucleotide sequence corresponding to the 3'end of SEQ ID 97, but excluding the poly (A) tail at the 3'end of SEQ ID 97. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 97 from nucleotide 40 to nucleotide 315, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 97 from nucleotide 40 to nucleotide 315, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 97 from nucleotide 40 to nucleotide 315. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 97 from nucleotide 124 to nucleotide 315, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 97 from nucleotide 124 to nucleotide 315, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 97 from nucleotide 124 to nucleotide 315.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 98; (b) a fragment of the amino acid sequence of SEQ ID 98, the fragment comprising eight contiguous amino acids of SEQ ID 98; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-368; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 98. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 98 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 98, or a protein comprising a fragment of the amino acid sequence of SEQ ID 98 having biological activity, the fragment comprising the amino acid sequence from amino acid 41 to amino acid 50 of SEQ ID 98.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 99; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 99 from nucleotide 70 to nucleotide 699; a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (d) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-368; a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO: 100; (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO: 100 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO: 100; (i) a polynucleotide which is an allelic variant of a

polynucleotide of above; a polynucleotide which encodes a species homologue of the protein of (g) or (h) above; (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in and (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (h) and that has a length that is at least 25% of the length of SEQ 99.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 99 from nucleotide 70 to nucleotide 699; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO: 100 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 100, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 100 having biological activity, the fragment comprising the amino acid sequence from amino acid 100 to amino acid 109 of SEQ ID NO: 100.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 99.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID 99, but excluding the poly (A) tail at the 3'end of SEQ ID 99; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA-368; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (ba) SEQ ID 99, but excluding the poly (A) tail at the 3'end of SEQ ID 99; and (bb) the nucleotide sequence of the insert of clone vr2_ 1 deposited with the ATCC under accession number PTA-368; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 99, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 99 to a nucleotide sequence corresponding to the 3'end of SEQ ID 99, but excluding the poly (A) tail at the 3'end of SEQ ID 99. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 99 from nucleotide 70 to nucleotide 699, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 99 from nucleotide 70 to nucleotide 699, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 99 from nucleotide 70 to nucleotide 699.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID NO: 100; (b) a fragment of the amino acid sequence of SEQ ID 100, the fragment comprising eight contiguous amino acids of SEQ ID NO: 100; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-368; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid

sequence of SEQ ID 100. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 100 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO: 100, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO: 100 having biological activity, the fragment comprising the amino acid sequence from amino acid 100 to amino acid 109 of SEQ ID 100.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 101; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID from nucleotide 170 to nucleotide 394; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID from nucleotide 227 to nucleotide (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone vc69_1 deposited with the ATCC under accession number PTA-1075; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; accession number PTA-1075; (g) a polynucleotide encoding a mature protein encoded by the 1075; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 102; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO: 102 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 102; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID NO:

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 101 from nucleotide 170 to nucleotide 394; the nucleotide sequence of SEQ ID NO: from nucleotide 227 to nucleotide the nucleotide sequence of the full-length number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of preferred embodiments, the polynucleotide encodes the full-length or a mature protein number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 102 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO: 102, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 102 having biological activity, the fragment comprising the amino acid sequence from amino acid 32 to amino acid 41 of SEQ ID NO: 102.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO:

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: SEQ ID NO: but excluding the poly (A) tail at the 3'end of SEQ ID and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA-1075; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe(s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID NO: but excluding the poly (A) tail at the 3'end of SEQ ID NO: and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 1075; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 101, and excluding the poly (A) tail at the 3'end of SEQ ID 101. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 101 from nucleotide 170 to nucleotide 394, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID NO: from nucleotide 170 to nucleotide 394, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID from nucleotide 170 to nucleotide 394. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID NO: from nucleotide 227 to nucleotide 394, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 101 from nucleotide 227 to nucleotide 394, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID NO: from nucleotide 227 to nucleotide 394.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 102; (b) a fragment of the amino acid sequence of SEQ ID 102, the fragment comprising eight contiguous amino acids of SEQ ID NO: 102; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; the protein being substantially free from other mammalian proteins. Preferably such embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 102 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO: 102, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO: 102 having biological activity, the fragment comprising the amino acid sequence from amino acid 32 to amino acid 41 of SEQ ID NO: 102.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 103; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 103 from nucleotide 43 to nucleotide 198; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 103 from nucleotide 85 to nucleotide 198; (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 1075; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO: 104; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO: 104 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 104; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least of the length of SEQ ID 103.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO: 103 from nucleotide 43 to nucleotide 198; the nucleotide sequence of SEQ ID NO: 103 from nucleotide 85 to nucleotide 198; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA- 1075; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone vc71_1 deposited with the ATCC under accession number PTA- 1075. In further preferred embodiments, the

present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO: 104 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 104, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 104 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO: 104.

Other embodiments provide the gene corresponding to the sequence of SEQ ID 103.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (aa) SEQ ID 103, but excluding the poly (A) tail at the 3'end of SEQ ID NO: 103; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA-1075; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (ba) SEQ ID NO: 103, but excluding the poly (A) tail at the 3'end of SEQ ID 103; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA-1075; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 103, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 103 to a nucleotide sequence corresponding to the 3'end of SEQ ID 103, but excluding the poly (A) tail at the 3'end of SEQ ID 103. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID NO: 103 from nucleotide 43 to nucleotide 198, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID NO: 103 from nucleotide 43 to nucleotide 198, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID NO: 103 from nucleotide 43 to nucleotide 198. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID NO: 103 from nucleotide 85 to nucleotide 198, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 103 from nucleotide 85 to nucleotide 198.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 104; (b) a fragment of the amino acid sequence of SEQ ID 104, the fragment comprising eight contiguous amino acids of SEQ ID NO: 104; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 104. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 104 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO: 104, or a protein comprising a fragment of the amino acid sequence of SEQ ID 104 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO: 104.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 105; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 105 from nucleotide 260 to nucleotide 1552; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 105 from nucleotide 335 to nucleotide 1552; (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 1075; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO: 106; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO: 106 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO: 106; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID 105.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 105 from nucleotide 260 to nucleotide 1552; the nucleotide sequence of SEQ ID 105 from nucleotide 335 to nucleotide 1552; the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 106 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO: 106, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 106 having biological activity, the fragment comprising the amino acid sequence from amino acid to amino acid 219 of SEQ ID 106.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 105.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (aa) SEQ ID NO: 105, but excluding the poly (A) tail at the 3'end of SEQ ID NO: 105; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 1075; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe(s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID NO: 105, but excluding the poly (A) tail at the 3'end of SEQ ID 105; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA-1075; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

corresponding to the sequence of SEQ ID 105, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 105 to a nucleotide sequence corresponding to the 3'end of SEQ ID 105, but excluding the poly (A) tail at the 3'end of SEQ ID 105. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 105 from nucleotide 260 to nucleotide 1552, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID NO: 105 from nucleotide 260 to nucleotide 1552, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID NO: 105 from nucleotide 260 to nucleotide 1552. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 105 from nucleotide 335 to nucleotide 1552, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 105 from nucleotide 335 to nucleotide 1552, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID NO: 105 from nucleotide 335 to nucleotide 1552.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 106; (b) a fragment of the amino acid sequence of SEQ ID 106, the fragment comprising eight contiguous amino acids of SEQ ID NO: 106; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 106. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 106 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO: 106, or a protein comprising a fragment of the amino acid sequence of SEQ ID 106 having biological activity, the fragment comprising the amino acid sequence from amino acid to amino acid 219 of SEQ ID NO: 106.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 107; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 107 from nucleotide 15 to nucleotide 320; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 107 from nucleotide 72 to nucleotide 320; (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo31_1 deposited with the ATCC under accession number PTA-1075; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (g) a polynucleotide encoding a mature protein encoded by the insert of clone vo31_1 deposited with the ATCC under accession number PTA- 1075; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 108; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO: 108 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 108; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least of the length of SEQ ID 107.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO: 107 from nucleotide 15 to nucleotide 320; the nucleotide sequence of SEQ ID NO: 107 from nucleotide 72 to nucleotide 320; the nucleotide sequence of the full-length protein coding sequence of clone vo31_1 deposited with the ATCC under accession number PTA- 1075; or the nucleotide sequence of a mature protein coding

sequence of clone deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone vo31_1 deposited with the ATCC under accession number PTA- 1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO: 108 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 108, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 108 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO: 108.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 107.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (aa) SEQ ID 107, but excluding the poly (A) tail at the 3'end of SEQ ID 107; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 1075; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe(s); and a process comprising the steps (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID NO: 107, but excluding the poly (A) tail at the 3'end of SEQ ID 107; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 1075; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 107, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 107 to a nucleotide sequence corresponding to the 3'end of SEQ ID 107, but excluding the poly (A) tail at the 3'end of SEQ ID 107. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence 320, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID NO: 107 from nucleotide 15 to nucleotide 320, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID NO: 107 from nucleotide 15 to nucleotide 320. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 107 from nucleotide 72 to nucleotide 320, and extending contiguously from a nucleotide 72 to nucleotide to a nucleotide sequence corresponding to the 3'end of

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: fragment comprising eight contiguous amino acids of SEQ ID NO: 108; and the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 108. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 108 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids ID NO: 108 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID 108.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ

ID 109; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 109 from nucleotide 38 to nucleotide 1255; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 109 from nucleotide 86 to nucleotide 1255; (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 1075; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO: 110; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 110 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO: 110; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least of the length of SEQ ID 109.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 109 from nucleotide 38 to nucleotide 1255; the nucleotide sequence of SEQ ID NO: 109 from nucleotide 86 to nucleotide 1255; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of preferred embodiments, the polynucleotide encodes the full-length or a mature protein number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 110 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO: 110, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 110 having biological activity, the fragment comprising the amino acid sequence from amino acid 198 to amino acid 207 of SEQ ID NO: 110.

Other embodiments provide the gene corresponding to the sequence of SEQ ID 109.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (aa) SEQ ID NO: 109, but excluding the poly (A) tail at the 3'end of SEQ ID 109; and (ab) the nucleotide sequence of the insert of clone 1075; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe(s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID 109, but excluding the poly (A) tail at the 3'end of SEQ ID NO: 109; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 1075; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 109, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 109 to a nucleotide sequence corresponding to the 3'end of SEQ ID 109, but excluding the poly (A) tail at the 3'end of SEQ ID 109. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence

of SEQ ID NO: 109 from nucleotide 38 to nucleotide 1255, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID NO: 109 from nucleotide 38 to nucleotide 1255, to sequence corresponding to the 3'end of said sequence of SEQ ID NO: 109 from nucleotide 38 to nucleotide 1255. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 109 from nucleotide 86 to nucleotide 1255, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID NO: 109 from nucleotide 86 to nucleotide 1255, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 109 from nucleotide 86 to nucleotide 1255.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID NO: 110; (b) a fragment of the amino acid sequence of SEQ ID 110, the fragment comprising eight contiguous amino acids of SEQ ID NO: 110; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 110. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 110 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO: 110, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO: 110 having biological activity, the fragment comprising the amino acid sequence from amino acid 198 to amino acid 207 of SEQ ID NO: 110.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 111; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 111 from nucleotide 80 to nucleotide 1276; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID 111 from nucleotide 131 to nucleotide 1276; (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 1075; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO: 112; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO: 112 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO: 112; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID NO: 111.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 111 from nucleotide 80 to nucleotide 1276; the nucleotide sequence of SEQ ID 111 from nucleotide 131 to nucleotide 1276; the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ

ID 112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO: 112, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 112 having biological activity, the fragment comprising the amino acid sequence from amino acid 194 to amino acid 203 of SEQ ID NO: 112.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 111.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID NO: but excluding the poly (A) tail at the 3'end of SEQ ID NO: 111; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 1075; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (ba) SEQ ID NO: 111, but excluding the poly (A) tail at the 3'end of SEQ ID NO: 111; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA-1075; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 111, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID excluding the poly (A) tail at the 3'end of SEQ ID 111. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID NO: 111 from nucleotide 80 to nucleotide 1276, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID NO: 111 from nucleotide 80 to nucleotide 1276, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID NO: 111 from nucleotide 80 to nucleotide 1276. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 111 from nucleotide 131 to nucleotide 1276, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID NO: 111 from nucleotide 131 to nucleotide 1276, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 111 from nucleotide 131 to nucleotide 1276.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 112; (b) a fragment of the amino acid sequence of SEQ ID 112, the fragment comprising eight contiguous amino acids of SEQ ID NO: 112; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 112. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ 112, comprising a fragment of the amino acid sequence of SEQ ID NO: 112 having biological activity, the fragment comprising the amino acid sequence from amino acid 194 to amino acid 203 of SEQ ID NO: 112.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide

selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 113; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 113 from nucleotide 202 to nucleotide 429; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 113 from nucleotide 292 to nucleotide 429; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone vq23_1 deposited with the ATCC under accession number PTA-1075; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 1075; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID 114; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO: 114 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO: 114; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID 113.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 113 from nucleotide 202 to nucleotide 429; the nucleotide sequence of SEQ ID NO: 113 from nucleotide 292 to nucleotide 429; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 114 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO: 114, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 114 having biological activity, the fragment comprising the amino acid sequence from amino acid 33 to amino acid 42 of SEQ ID NO: 114.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 113.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting (a) a process comprising the steps (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (aa) SEQ ID NO: 113, but excluding the poly (A) tail at the 3'end of SEQ ID 113; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 1075; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID NO: but excluding the poly (A) tail at the 3'end of SEQ ID 113; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 1075; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 113, and extending contiguously from a nucleotide sequence

corresponding to the 5'end of SEQ ID 113 to a nucleotide sequence corresponding to the 3'end of SEQ ID 113, but excluding the poly (A) tail at the 3'end of SEQ ID 113. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 113 from nucleotide 202 to nucleotide 429, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID NO: 113 from nucleotide 202 to nucleotide 429, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID 113 from nucleotide 202 to nucleotide 429. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID NO: 113 from nucleotide 292 to nucleotide 429, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 113 from nucleotide 292 to nucleotide 429, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID NO: 113 from nucleotide 292 to nucleotide 429.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID NO: 114; (b) a fragment of the amino acid sequence of SEQ ID 114, the fragment comprising eight contiguous amino acids of SEQ ID 114; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 114. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 114 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO: 114, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO: 114 having biological activity, the fragment comprising the amino acid sequence from amino acid 33 to amino acid 42 of SEQ ID NO: 114.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 115; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 115 from nucleotide 37 to nucleotide 1113; a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 115 from nucleotide 88 to nucleotide 1113; (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq24_1 deposited with the ATCC under accession number PTA-1075; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone vq24_1 deposited with the ATCC under accession number PTA-1075; protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 1075; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO: 116; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO: 116 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO: 116; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID 115.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 115 from nucleotide 37 to nucleotide 1113; the nucleotide sequence of SEQ ID NO: 115 from nucleotide 88 to nucleotide 1113; the nucleotide sequence of the full-length protein coding sequence of clone vq24_1 deposited with the ATCC under accession number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA

insert of clone deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 116 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO: 116, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 116 having biological activity, the fragment comprising the amino acid sequence from amino acid 174 to amino acid 183 of SEQ ID NO: 116.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 115.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (aa) SEQ ID NO: 115, but excluding the poly (A) tail at the 3'end of SEQ ID 115; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA- 1075; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (ba) SEQ ID NO: but excluding the poly (A) tail at the 3'end of SEQ ID NO: 115; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA-1075; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 115, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 115 to a nucleotide sequence corresponding to the 3'end of SEQ ID 115, but excluding the poly (A) tail at the 3'end of SEQ ID 115. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID NO: 115 from nucleotide 37 to nucleotide 1113, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID NO: 115 from nucleotide 37 to nucleotide 1113, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID NO: 115 from nucleotide 37 to nucleotide 1113. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 115 from nucleotide 88 to nucleotide 1113, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID NO: 115 from nucleotide 88 to nucleotide 1113, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID NO: 115 from nucleotide 88 to nucleotide 1113.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID NO: 116; (b) a fragment of the amino acid sequence of SEQ ID 116, the fragment comprising eight contiguous amino acids of SEQ ID NO: 116; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 116. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 116 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO: 116, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO: 116 having biological activity, the fragment comprising the amino acid sequence from amino acid

174 to amino acid 183 of SEQ ID 116.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 117; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 117 from nucleotide 40 to nucleotide 207; (c) a polynucleotide comprising the nucleotide sequence of SEQ ID (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 1075; (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO: 118; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO: 118 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO: a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; (1) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least of the length of SEQ ID 117.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO: 117 from nucleotide 40 to nucleotide 207; the nucleotide sequence of SEQ ID NO: 117 from nucleotide 103 to nucleotide 207; the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA- 1075; or the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO: 118 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID 118, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 118 having biological activity, the fragment comprising the amino acid sequence from amino acid 23 to amino acid 32 of SEQ ID 118.

Other embodiments provide the gene corresponding to the sequence of SEQ ID NO: 117.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of: (a) a process comprising the steps of: (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of: (aa) SEQ ID 117, but excluding the poly (A) tail at the 3'end of SEQ ID 117; and (ab) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA-1075; (ii) hybridizing said probe (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and (iii) isolating the DNA polynucleotides detected with the probe (s); and (b) a process comprising the steps of: (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting (ba) SEQ ID NO: 117, but excluding the poly (A) tail at the 3'end of SEQ ID NO: 117; and (bb) the nucleotide sequence of the insert of clone deposited with the ATCC under accession number PTA-1075; (ii) hybridizing said primer (s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; (iii) amplifying human DNA sequences; and (iv) isolating the polynucleotide products of step (b) (iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID 117, and extending contiguously from a nucleotide sequence corresponding to the 5'end of SEQ ID 117 to a nucleotide sequence corresponding to the 3'end of SEQ ID but excluding the poly (A) tail at the 3'end of SEQ ID 117. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID NO: 117 from nucleotide 40 to nucleotide 207, and extending contiguously from a nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID NO: 117 from nucleotide 40 to nucleotide 207, to a nucleotide sequence corresponding to the 3'end of said sequence 117 from nucleotide 40 to nucleotide 207. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the sequence of SEQ ID nucleotide sequence corresponding to the 5'end of said sequence of SEQ ID 117 from nucleotide 103 to nucleotide 207, to a nucleotide sequence corresponding to the 3'end of said sequence of SEQ ID NO: 117 from nucleotide 103 to nucleotide 207.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID NO: 118; (b) a fragment of the amino acid sequence of SEQ ID 118, the fragment comprising eight contiguous amino acids of SEQ ID NO: 118; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID 118. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID 118 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO: 118, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO: 118 having biological activity, the fragment comprising the amino acid sequence from amino acid 23 to amino acid 32 of SEQ ID NO: 118.

In certain preferred embodiments, the polynucleotide is operably linked to an expression control sequence. The invention also provides a host cell, including bacterial, yeast, insect and mammalian cells, transformed with such polynucleotide compositions.

Also provided by the present invention are organisms that have enhanced, reduced, or modified expression of the gene (s) corresponding to the polynucleotide sequences disclosed herein.

Processes are also provided for producing a protein, which comprise: (a) growing a culture of the host cell transformed with such polynucleotide compositions in a suitable culture medium; and (b) purifying the protein from the culture.

The protein produced according to such methods is also provided by the present invention.

Protein compositions of the present invention may further comprise a pharmaceutically acceptable carrier. Compositions comprising an antibody which specifically reacts with such protein are also provided by the present invention.

Methods are also provided for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of a composition comprising a protein of the present invention and a pharmaceutically acceptable

DESCRIPTION OF THE DRAWINGS Figures and representations of the pED6 and pNOTs vectors, respectively, used for deposit of clones disclosed herein.

DETAILED DESCRIPTION ISOLATED PROTEINS AND POLYNUCLEOTIDES Nucleotide and amino acid sequences, as presently determined, are reported below of each clone be determined by sequencing of the deposited clone in accordance with known methods. The predicted amino acid sequence (both full-length and mature forms'can then be determined from such nucleotide sequence. The amino acid sequence of the protein encoded by a particular clone can also be determined by expression of the clone in a suitable host cell, collecting the protein and determining its sequence. For each disclosed protein applicants have identified what they have determined to be the reading frame best identifiable with sequence information available at the time of filing.

As used herein a"secreted"protein is one which, when expressed in a suitable host cell, is across or through a membrane, including transport as a result of signal sequences in its amino acid sequence."Secreted"proteins include without limitation proteins secreted wholly (e. g., soluble proteins) or partially (e. g., receptors) from the cell in which they are expressed."Secreted"proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

Clone"vc62 A polynucleotide of the present invention has been identified as was isolated from a human fetal brain library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID 1, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 2. Amino acids 3 to 15 of SEQ ID 2 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 16. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein. If the 'G'residue at position 254 of SEQ ID NO: 1 were deleted, another potential reading frame and predicted amino acid sequence that would then be encoded by nucleotides 27 to 365 of SEQ ID NO: is reported in SEQ ID NO: 169.

The restriction fragment obtainable from the deposit containing clone should be approximately 4221 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AA580489 sl Homo sapiens clone IMAGE 1084602, sequence), AF047042 (Homo sapiens citrate synthase complete cds), and T04200 (Sugar beet citrate synthase standard; to The predicted amino acid sequence disclosed herein for was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted protein demonstrated at least some similarity to sequences identified as AF047042 (citrate synthase [Homo sapiens]) and R82839 (Sugar beet citrate synthase). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity.

Clone"vplO 1" A polynucleotide of the present invention has been identified as was isolated from a human adult prostate library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in 3, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 4. Amino acids 19 to

31 of SEQ ID 4 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 32. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vpl0_1 protein. If another'G'residue were inserted in 3 after the'G'residue at position 868, another potential reading frame and predicted amino acid sequence that would be encoded by what would then be nucleotides 6 to 968 of 3 is reported in SEQ ID NO: 170.

The restriction fragment obtainable from the deposit containing clone vpl0_1 should be approximately 1401 bp.

The nucleotide sequence disclosed herein for vpl0_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vpl0_1 demonstrated at least some similarity with sequences identified as AA733074 sl Soares fetal heart NbHH19W Homo sapiens clone 399565 3'similar to WP: C15H9.5 CE06834; sequence). The predicted amino acid sequence disclosed herein for vpl0_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted protein demonstrated at least some similarity to the sequence identified as U56965 (unknown protein [Caenorhabditis elegans]). Based upon sequence similarity, vpl0_1 proteins and each similar protein or peptide may share at least some activity. The computer program predicts a potential transmembrane domain within the vpl0_1 protein sequence centered around amino acid 270 of SEQ ID 4.

A polynucleotide of the present invention has been identified as clone"vpl 11_1". vp11_1 was isolated from a human adult prostate library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vpl is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as"vpl protein").

The nucleotide sequence presently determined is reported in SEQ ID and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vpl protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 6. Amino acids 5 to 17 of SEQ ID 6 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vpl protein.

The restriction fragment obtainable from the deposit containing clone vpl 1_1 should be approximately 1329 bp.

The nucleotide sequence disclosed herein for vp11_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database.

Clone"vpl3 1" A polynucleotide of the present invention has been identified as vpl3_1 was isolated from a human adult prostate library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp13_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as"vpl3_1 protein").

7, and includes a poly (A) tail. What applicants presently believe to be the proper to the foregoing nucleotide sequence is reported in SEQ ID 8. Amino acids 13 to 25 of SEQ ID 8 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26. Due

to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vpl3_1 protein.

Other potential vpl3_1 reading frames and predicted amino acid sequences are encoded by nucleotides 151 to 267 of SEQ ID 7, with the encoded amino acid sequence reported in SEQ ID and by nucleotides 209 to 787 of SEQ ID 7, with the encoded amino acid sequence reported in SEQ ID NO: 172. Amino acids 1 to 13 of SEQ ID 172 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 14. Due to the hydrophobic nature of this predicted leader/signal sequence, it is likely to act as a transmembrane domain should it not be separated from the remainder of the protein of SEQ ID 172. The protein of SEQ ID 172 also demonstrates significant homology to the human Notch protein, Delta proteins from various species, and other EGF-repeat-containing transmembrane proteins. A deletion or insertion causing a frame-shift in the nucleotide sequence of SEQ ID 7 in the region approximately between nucleotides 208 and 267 of SEQ ID 7 could join the reading frames of SEQ ID 171 and SEQ ID 172 into a single reading frame encoding an EGF-repeat-containing protein. Further, the region approximately between nucleotides 605 and 850 may be an alternatively spliced exon.

If the'A'residue at position 423 of SEQ ID 7 were deleted, another potential reading frame and predicted amino acid sequence that would be encoded by what would then be nucleotides 288 to 503 of SEQ ID 7 is reported in SEQ ID NO: 173.

The restriction fragment obtainable from the deposit containing clone vpl3_1 should be approximately 1048 bp.

The nucleotide sequence disclosed herein for vpl3_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vpl3_1 demonstrated at least some similarity with sequences identified as AA190865 sl s3 937216 Homo sapiens clone 626955 3'similar to TR G1336628 G1336628 EGF REPEAT TRANSMEMBRANE PROTEIN; sequence), and U57368 (Mus musculus EGF repeat transmembrane protein complete cds). The predicted amino acid sequence disclosed herein for vpl3_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted protein demonstrated at least some similarity to sequences identified as AC004663 (Notch 3 [Homo sapiens]), R28960 (Delta Dl 1), and U57368 (EGF repeat transmembrane protein [Mus musculus]). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity. The computer program predicts a potential transmembrane domain within the protein sequence centered around amino acid 56 of SEQ ID N0: 8.

A polynucleotide of the present invention has been identified as vpl6_1 was isolated from a human adult prostate library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vpl6_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID 9, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO: 10. Amino acids 34 to 46 of SEQ ID NO: 10 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 47. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vpl6_1 protein.

Another potential vp reading frame and predicted amino acid sequence is encoded by basepairs 1621 to 1839 of SEQ ID 9 and is reported in SEQ ID 174.

The restriction fragment obtainable from the deposit containing clone vpl6_1 should be approximately 2105 bp.

The nucleotide sequence disclosed herein for vpl6_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vpl6_1 demonstrated at least some similarity with sequences identified as AA523851 Homo sapiens clone IMAGE: sequence). Based upon sequence similarity, vpl6_1 proteins and each similar protein or peptide may share at least some activity. The computer program predicts two potential transmembrane domains within the vpl6_1 protein sequence, one centered around amino acid 36 and another around amino acid 69 of SEQ ID 10. The nucleotide sequence of vpl6_1 indicates that it may contain an Alu repetitive element.

A polynucleotide of the present invention has been identified as vp21_1 was isolated from a human adult prostate library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence of as presently determined is reported in SEQ ID 11, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp21_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 12. Amino acids 62 to 74 of SEQ ID NO: 12 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 75. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp21_1 protein.

Another potential vp21_1 reading frame and predicted amino acid sequence encoded by basepairs 598 to 831 of SEQ ID NO: 11 is reported in SEQ ID NO: 175. Amino acids 1 to 6 of SEQ ID 175 and amino acids 41 to 43 of SEQ ID 175 are predicted leader/signal sequences, with the predicted mature amino acid sequences beginning at amino acid 7 or at amino acid 44, respectively.

The restriction fragment obtainable from the deposit containing clone vp21_1 should be approximately 1538 bp.

The nucleotide sequence disclosed herein for vp21_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp21_1 demonstrated at least some similarity with sequences identified as AC004076 (Homo sapiens chromosome 19, cosmid R30217, complete sequence). The predicted amino acid sequence disclosed herein for vp21_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vp21_1 protein demonstrated at least some similarity to sequences identified as (Zinc finger protein F18547_1 [Homo sapiens]) and sequence similarity, proteins and each similar protein or peptide may share at least some activity. The computer program predicts potential transmembrane domains within the predicted vp21 _ 1 protein sequences, one centered around amino acid 70 of SEQ ID NO: 12, and one centered around amino acid 17 of SEQ ID 175.

A polynucleotide of the present invention has been identified as was isolated from a human adult prostate library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp22_1 is a full-length clone,

including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID 13, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp22_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO: 14. Amino acids 13 to 25 of SEQ ID NO: 14 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

Another potential reading frame and predicted amino acid sequence encoded by basepairs 408 to 1154 of SEQ ID NO: 13 is reported in SEQ ID NO: 176. Amino acids 40 to 52 of SEQ ID NO: 176 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 53. Due to the hydrophobic nature of this predicted leader/signal sequence, it is likely to act as a transmembrane domain should it not be separated from the remainder of the protein of SEQ ID 176. A frameshift within the nucleotide sequence of SEQ ID NO: 13 approximately between nucleotides 163 and 477 could join the openreading frames of SEQ ID NO: 14 and SEQ ID 176.

The restriction fragment obtainable from the deposit containing clone should be approximately 1718 bp.

The nucleotide sequence disclosed herein for vp22_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp22_1 demonstrated at least some similarity with sequences identified as AA526186 Homo sapiens clone IMAGE: 984533, sequence), AA570505 (nk64hOl. sl NCI_CGAP_Schl Homo sapiens clone IMAGE 1018321, sequence), AB006085 (Danio rerio mRNA for MINDIN2, complete cds), and T78360 (Human neuronal attachment factor-1 DNA; standard; DNA). The predicted amino acid sequence disclosed herein for vp22_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vp22_1 protein demonstrated at least some similarity to sequences identified as AB006085 (MINDIN2 [Danio rerio]) and W23663 (Human neuronal attachment Based upon sequence similarity, vp22_1 proteins and each similar protein or peptide may share at least some activity.

A polynucleotide of the present invention has been identified as vq2_1 was isolated from a human adult lung library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq2_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence of vq2_1 as presently determined is reported in SEQ ID 15, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO: 16. Amino acids 4 to 16 of SEQ ID NO: 16 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 17. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

The restriction fragment obtainable from the deposit containing clone should be approximately 896 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq2_1 demonstrated at least some similarity with sequences identified as (qe76hO5. Homo sapiens clone

IMAGE: 1744953 3', sequence) (Human haematopoietic-specific protein (HSP) DNA; standard; DNA). The predicted amino acid sequence disclosed herein for was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted protein demonstrated at least some similarity to the sequence identified as W35904 (Human haematopoietic-specific protein (HSP)). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity.

1" A polynucleotide of the present invention has been identified as vq3_1 was isolated from a human adult lung library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq3_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence of vq3_1 as presently determined is reported in SEQ ID 17, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO: 18. Amino acids 11 to 23 of SEQ ID NO: 18 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

The restriction fragment obtainable from the deposit containing clone should be approximately 1490 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the database. The nucleotide sequence indicates that it may contain an Alu repetitive element.

A polynucleotide of the present invention has been identified as vq5_1 was isolated from a human adult lung library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence of vq5_1 as presently determined is reported in SEQ ID and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 20. Amino acids 9 to 21 of SEQ ID 20 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

The restriction fragment obtainable from the deposit containing clone should be approximately 2207 bp.

The nucleotide sequence disclosed herein for vq5_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AQ036276 TF CIT-HSP Homo sapiens genomic clone survey sequence) standard; to mRNAP). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity. The computer program predicts that the signal sequence at residue 22 of SEQ ID 20 is also a potential transmembrane domain.

A polynucleotide of the present invention has been identified as was isolated from a human adult lung

library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID 21, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 22. Amino acids 6 to 18 of SEQ ID 22 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

The restriction fragment obtainable from the deposit containing clone should be approximately 1875 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AA729043 Homo sapiens clone IMAGE: 1241201 similar to contains Alu repetitive element; sequence). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity. The computer program predicts an additional potential transmembrane domain within the protein sequence centered around amino acid 37 of SEQ ID 22. The nucleotide sequence of indicates that it may contain an Alu repetitive element.

A polynucleotide of the present invention has been identified as vrl_1 was isolated from a human adult muscle library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vrl_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as"vrl_1 protein").

The nucleotide sequence of vrl_1 as presently determined is reported in SEQ ID 23, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 24. Amino acids 34 to 46 of SEQ ID 24 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 47. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein. The region of SEQ ID 23 approximately between nucleotides 1931 and 1977 of SEQ ID 23 may be an alternatively spliced exon.

The restriction fragment obtainable from the deposit containing clone should be approximately 1512 bp.

The nucleotide sequence disclosed herein for vrl_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AL031602 (Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1174N9; HTGS phase 1), I64695 (Sequence 1 from patent US 5665588), and T35233 (Natural killer lytic associated protein standard; cDNA). The predicted amino acid sequence disclosed herein for vrl_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vrl_1 protein demonstrated at least some similarity to sequences identified as R99256 (GEG-154 gene product [Mus musculus]). Based upon sequence similarity, vrl_1 proteins and each similar protein or peptide may share at least some activity. The computer program predicts an additional potential transmembrane domain within the protein sequence centered around amino acid 150 of SEQ ID 24.

Clone"vc63 A polynucleotide of the present invention has been identified as was isolated from a human fetal brain library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID 25, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 26. Another potential 1100 of SEQ ID 25 is reported in SEQ ID NO: 177. Amino acids 140 to 152 of SEQ ID 177 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 153. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO: 177.

The restriction fragment obtainable from the deposit containing clone should be approximately 2397 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as N66555 sl Homo sapiens clone 278773 3') and T21367 (Human gene signature HUMGS02731; standard; to The predicted amino acid sequence disclosed herein for was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted protein demonstrated at least some similarity to the sequence identified as Z36948 (D2089.2 [Caenorhabditis elegans]). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity. The computer program predicts a potential transmembrane domain within the protein sequence of SEQ ID NO: 177, centered around amino acid 153 of SEQ ID NO: 177.

Clone"vb25 A polynucleotide of the present invention has been identified as vb25_1 was isolated from a human fetal brain library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID 27, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb25_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 28. Amino acids 5 to 17 of SEQ ID 28 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

The restriction fragment obtainable from the deposit containing clone should be approximately 1677 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as Z73429 (Human DNA sequence from cosmid cN32F9 on chromosome 22ql sequence similarity, vb25_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence indicates that it may contain one or more of the following repetitive elements: AC simple repeat, AG simple repeat, ALU, MIR.

Clone"vb27 A polynucleotide of the present invention has been identified as vb27_1 was isolated from a

human fetal library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID 29, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 30. Amino acids 14 to 26 of SEQ ID 30 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 27. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vb27_1 protein.

The restriction fragment obtainable from the deposit containing clone should be approximately 3456 bp.

The nucleotide sequence disclosed herein for vb27_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AC005035 (Homo sapiens BAC clone NH0353P23 from 2, complete sequence) and H73579 rl Homo sapiens clone Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence indicates that it may contain one or mor of the following repetitive elements: ALU, Mer3.

Clone"vb28 1" A polynucleotide of the present invention has been identified as was isolated from a human fetal brain library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb28_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 32. Amino acids 4 to 16 of SEQ ID 32 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 17. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vb28_1 protein.

The restriction fragment obtainable from the deposit containing clone should be approximately 3008 bp.

The nucleotide sequence disclosed herein for vb28_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AA046671 sapiens clone IMAGE: 376721 5'similar to PIR: A38745 A38745 cell adhesion molecule CD44 precursor-rat; sequence) and V22687 (DNA encoding a CD44-like protein). The predicted amino acid sequence disclosed herein for was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. protein demonstrated at least some similarity to sequences identified as W56249 (Amino acid sequence of a CD44-like protein) and X66081 (CD44 [Mus musculus]). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity.

Clone"vb29 A polynucleotide of the present invention has been identified as was isolated from a human fetal brain library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID 33, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 34. Amino acids 11 to 23 of SEQ ID 34 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

The restriction fragment obtainable from the deposit containing clone should be approximately 2970 bp.

The nucleotide sequence disclosed herein for vb29_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AA084068 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens clone 547607 5', sequence) and AQ418918 TV RPCI-11 Homo sapiens genomic clone survey sequence). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity. The computer program predicts a potential transmembrane domain within the vb29_1 protein sequence centered around amino acid 41 of SEQ ID 34. The nucleotide sequence of vb29_1 indicates that it may contain an Alu repetitive element.

Clone"vb30 A polynucleotide of the present invention has been identified as was isolated from a human fetal brain library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb30_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID 35, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 36. Amino acids 15 to 27 of SEQ ID 36 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 28. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

The restriction fragment obtainable from the deposit containing clone should be approximately 3325 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the databases. The nucleotide sequence indicates that it may contain an Alu repetitive element.

Clone"vc67 A polynucleotide of the present invention has been identified as was isolated from a human fetal brain library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID 37, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc67_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 38. Another potential reading frame and predicted amino acid sequence encoded by basepairs 3 to 242 of SEQ ID 37 is reported in SEQ ID NO: 178.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone should be approximately 2305 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as T23222 (Human gene signature HUMGS05018), W87297 sl Homo sapiens clone IMAGE 417173 3', sequence), and Z97201 (Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 94M16, WORKING DRAFT SEQUENCE). The predicted amino acid sequence disclosed herein for was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted protein demonstrated at least some similarity to sequences identified as W69427 (Human secreted protein and Z68751 (Similarity to Yeast hypothetical protein YKKO (SW EST EMBL C12578 comes from this gene; EST comes from this gene; EST Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity. The computer program predicts two potential transmembrane domains within the vc67_1 protein sequence of SEQ ID 38, one centered around amino acid 58 and another around amino acid 85 of SEQ ID 38.

Clone"vf4 A polynucleotide of the present invention has been identified as vf4_1 was isolated from a human adult heart library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vf4_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence of vf4_1 as presently determined is reported in SEQ ID 39, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 40. Amino acids 5 to 17 of SEQ ID 40 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

The restriction fragment obtainable from the deposit containing clone should be approximately 972 bp.

The nucleotide sequence disclosed herein for vf4_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AA813690 Homo sapiens clone 1376248 3', sequence) and V86544 (EST clone AZ285). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity.

A polynucleotide of the present invention has been identified as was isolated from a human adult brain library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence of as presently determined is reported in SEQ ID 41, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 42. Amino acids 13 to 25 of SEQ ID 42 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

The restriction fragment obtainable from the deposit containing clone should be approximately 3667 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as xl Homo sapiens clone IMAGE 1892323 3', sequence). The predicted amino acid sequence disclosed herein for was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted protein demonstrated at least some similarity to sequences identified as U53155 (ZC513.5 [Caenorhabditis elegans]). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity. The computer program predicts the following transmembrane domains within the vg3_1 protein sequence: four certain transmembrane domains centered around amino acids 78,133,156, and 298 of SEQ ID 42, respectively; four strongly putative transmembrane domains centered around amino acids 105,189,221, and 354 of SEQ ID 42, respectively; and six possible transmembrane domains centered around amino acids 262,272,322,367,432, and 460 of SEQ ID 42, respectively. Motifs analysis detected a Crystallins beta and gamma'Greek key'motif signature around amino acid 52 of SEQ ID 42. The nucleotide sequence of indicates that it may contain an Alu repetitive element.

Clone"vo2 1" A polynucleotide of the present invention has been identified as was isolated from a human adult pancreas library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo2_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence of as presently determined is reported in SEQ ID 43, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 44.

Another potential vo2_1 reading frame and predicted amino acid sequence encoded by basepairs 95 to 280 of SEQ ID 43 is reported in SEQ ID NO: 179. Amino acids 9 to 21 of SEQ ID NO: 179 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO: 179.

reading frame and predicted amino acid sequence encoded by basepairs 76 to 258 of SEQ ID 43 is reported in SEQ ID NO: 180. Amino acids 18 to 30 of SEQ ID NO: 180 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid Due to the hydrophobic nature of this predicted leader/signal sequence, it is likely to act as a transmembrane domain should it not be separated from the remainder of the protein of SEQ ID NO: 180.

Another potential vo2_ 1 reading frame and predicted amino acid sequence encoded by basepairs 2131 to 2310 of SEQ ID N0: 43 is reported in SEQ ID NO: Amino acids 38 to 50 of SEQ ID 181 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 11; amino acids 19 to 31 of SEQ ID NO: 181 are also a possible leader/signal sequence, with the predicted mature amino acid sequence in this case beginning at amino acid 32. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the protein of SEQ ID NO:

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone should be approximately 2903 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as Homo sapiens clone IMAGE 1670293 3', sequence). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity.

Clone"vo3 A polynucleotide of the present invention has been identified as was isolated from a human adult pancreas library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the 45, and includes a poly (A) tail. What applicants presently believe to be the proper to the foregoing nucleotide sequence is reported in SEQ ID 46. Amino acids 107 to of SEQ ID 46 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 120. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the

If a"C"residue were to be deleted from the nucleotide sequence of SEQ ID 45 at either position 917 or position 918, reading frame and predicted amino acid sequence encoded by what would then be basepairs 697 to 1377 of SEQ ID 45 is reported in SEQ ID 182. Amino acids 62 to 74 of SEQ ID 182 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 75. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO: 182.

The restriction fragment obtainable from the deposit containing clone should be approximately 1592 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AA530997 Homo sapiens clone IMAGE: 985618 3', sequence), AA683481 sl Soares pregnant uterus Homo sapiens clone IMAGE: 505805 3', sequence), D88158 (Pig for cytochrome b561, complete cds), and V84516 (Human secreted protein gene 106 clone The predicted amino acid sequence disclosed herein for was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted protein demonstrated at least some similarity to sequences identified as U06715 (HCYTO B561 [Homo sapiens]) and W89024 (Polypeptide fragment encoded by gene 156). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity. The computer program predicts five potential transmembrane domains within the protein sequence, centered around amino acids 35,75,113,146, and 191 of SEQ ID 46, respectively.

1" A polynucleotide of the present invention has been identified as clone"vo5_1". vo5_1 was isolated from a human adult pancreas library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo5_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as"vo5_1 protein").

The nucleotide sequence of as presently determined is reported in SEQ ID 47, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 48. Amino acids 8 to 20 of SEQ ID 48 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

The restriction fragment obtainable from the deposit containing clone should be approximately 2487 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo5_1 demonstrated at least some similarity with sequences identified as AA868551 sl Soares testis NHT Homo sapiens clone IMAGE: 1408745 3', sequence) and AC005500 (complete sequence [Homo sapiens Chromosome PAC Clone In DGCR Region]). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence ofvo5_1 indicates that it may contain an Alu repetitive element.

Clone"vo6 A polynucleotide of the present invention has been identified as vo6_1 was isolated from a human adult pancreas library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence of vo6_1 as presently determined is reported in SEQ ID 49, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 50. Amino acids 77 to 89 of SEQ ID 50 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 90. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

The restriction fragment obtainable from the deposit containing clone should be approximately 1272 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AL020989 (Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 192P9; HTGS phase 1), T34592 nerve protein coding sequence), and U 13617 (Rattus norvegicus Sprague-Dawley plasmolipin complete cds). The predicted amino acid sequence disclosed herein for was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol.

The predicted protein demonstrated at least some similarity to sequences identified as R99799 nerve protein, facilitates regeneration of nerve cells) and U13617 (plasmolipin [Rattus norvegicus]). Plasmolipin is an 18-kDa proteolipid protein found in kidney and brain, where it is restricted to the apical surface of tubular epithelial cells and to mammalian myelinated tracts, respectively; addition of plasmolipin to lipid bilayers induces the formation of ion channels, which are voltage-dependent and K (+)-selective.

(See Fischer and Sapirstein, 1994, J. Biol. Chem. 269 (40): 24912-24919, which is incorporated by reference herein). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity. The computer program predicts three potential transmembrane domains within the protein sequence, centered around amino acids 14,42, and 90 of SEQ ID 50, respectively.

Clone"vo9 A polynucleotide of the present invention has been identified as was isolated from a human adult pancreas library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo9_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence of as presently determined is reported in SEQ ID and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 52. Amino acids 22 to 34 of SEQ ID NO: are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 35. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

The restriction fragment obtainable from the deposit containing clone should be approximately 3331 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo9_1 demonstrated at least some similarity with sequences identified as AA936961 s1 NCI_CGAP_GC4 Homo sapiens clone IMAGE 1571071 3', sequence), AF010496 9Rhodobacter capsulatus strain partial genome), AL035661 (Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone WORKING DRAFT SEQUENCE), and Q24673 gene). The predicted amino acid sequence disclosed herein for was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted protein demonstrated at least some similarity to sequences identified as R23968 gene product) and Y15417 (acetate--CoA ligase [Coprinus cinereus]). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity.

A polynucleotide of the present invention has been identified as clone"vol vol was isolated from a human adult pancreas library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vol 1_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as"vol 1_1 protein").

The nucleotide sequence presently determined is reported in SEQ ID 53, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vol protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 54. Amino acids 52 to 64 of SEQ ID 54 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 65.

Another potential reading frame and predicted amino acid sequence, encoded by basepairs 53, 183. Amino acids 10 to 22 of SEQ ID NO: 183 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID 183.

The restriction fragment obtainable from the deposit containing clone vol should be approximately 1509 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vol demonstrated at least some similarity with sequences identified as D83866 (similar to none, sequence). Based upon sequence similarity, vol 1_1 proteins and each similar protein or peptide may share at least some activity.

A polynucleotide of the present invention has been identified as was isolated from a human adult pancreas library and was identified as encoding a secreted or transmembrane protein on the basis of

computer analysis of the amino acid sequence of the encoded protein. vol2_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID 55, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino, acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 56. Amino acids 4 to 16 of SEQ ID 56 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 17.

Another potential reading frame and predicted amino acid sequence, encoded by basepairs 107 to of SEQ ID 55, is reported in SEQ ID 184.

Amino acids 14 to 26 and amino acids 18 to 30 of SEQ ID 184 are predicted leader/signal sequences, with the predicted mature amino acid sequence beginning at amino acid 27 or at amino acid respectively. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO: 184.

The restriction fragment obtainable from the deposit containing clone should be approximately 986 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AA444152 rl Soares testis NHT Homo sapiens clone 757210 5', sequence). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity. The computer program predicts a potential transmembrane domain within the protein sequence centered around amino acid 51 of SEQ ID 56.

A polynucleotide of the present invention has been identified as vol3_1 was isolated from a human adult pancreas library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. The clone includes coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID 57, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo 13_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 58. Amino acids 8 to 20 of SEQ ID 58 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21.

The restriction fragment obtainable from the deposit containing clone vo13_1 should be approximately 1073 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AA988298 Homo sapiens clone IMAGE: 1607018 3', sequence) and V69614 (Human secreted protein gene 4 clone HE8ND56). The predicted amino acid sequence disclosed herein was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo13_1 protein demonstrated at least some similarity to sequences identified as W83934 (Human secreted protein from gene 4 clone HE8ND56).

Based upon sequence similarity, proteins and each similar protein or peptide may share at least some

activity. The computer program predicts a potential transmembrane domain within the protein sequence centered around amino acid 50 of SEQ ID NO: 58.

A polynucleotide of the present invention has been identified as vo14_1 was isolated from a human adult pancreas library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. volais a full-length clone, including the 59, and includes a poly (A) tail. What applicants presently believe to be the proper to the foregoing nucleotide sequence is reported in SEQ ID 60. Amino acids 14 to 26 of SEQ ID 60 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 27.

The restriction fragment obtainable from the deposit containing clone

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the databases. Based upon sequence similarity, vo 14_ 1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of indicates that it may contain one or more of the following repetitive elements: Alu, TAAAA repeat.

A polynucleotide of the present invention has been identified as was isolated from a human adult pancreas library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as"vol5_1 protein").

The nucleotide sequence presently determined is reported in SEQ ID 61, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vol5_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 62. Amino acids 13 to 25 of SEQ ID 62 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26.

If a nucleotide were deleted between nucleotide and nucleotide 460 of SEQ ID 61, another potential reading frame and predicted amino acid sequence, encoded by what would then be basepairs 90 to of SEQ ID is reported in SEQ ID 185. Amino acids 16 to 28 and amino acids 13 to 25 of SEQ ID 185 are predicted leader/signal sequences, with the predicted mature amino acid sequence beginning at amino acid 29 or at amino acid 26, respectively. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO: 185.

The restriction fragment obtainable from the deposit containing clone should be approximately 2842 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AI096756 xl Homo sapiens clone IMAGE 1703178 3', sequence). Based upon sequence similarity, vol5_1 proteins and each similar protein or peptide may share at least some activity. The computer program predicts a potential transmembrane domain within the protein sequence centered around amino acid 126 of SEQ ID 62. The nucleotide sequence of indicates that it may contain one ore more repeat sequences.

1" A polynucleotide of the present invention has been identified as vol6_1 was isolated from a human adult pancreas library and was identified as encoding a secreted or transmembrane protein on the basis

of computer analysis of the amino acid sequence of the encoded protein. vol6_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID 63, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 64. Amino acids 51 to 63 of SEQ ID 64 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 64. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

If an"A"or"G"nucleotide were inserted between nucleotides 102 and 103of SEQ ID 63 and an additional"A"residue inserted between nucleotides 271 and 273 of SEQ ID 63, another potential reading frame and predicted amino acid sequence, encoded by what would then be basepairs 6 to 338 of SEQ ID 63, is reported in SEQ ID NO:. Amino acids 5 to 17 and amino acids 4 to 16 of SEQ ID NO: 186 are predicted leader/signal sequences, with the predicted mature amino acid sequence beginning at amino acid 18 or at amino acid 17, respectively. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID 186.

Another potential reading frame and predicted amino acid sequence, encoded by basepairs 846 to 1061 of SEQ ID 63, is reported in SEQ ID 187.

Amino acids 12 to 24 and amino acids 11 to 23 of SEQ ID 187 are predicted leader/signal sequences, with the predicted mature amino acid sequence beginning at amino acid 25 or at amino acid 24, respectively. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO: 187.

Nucleotides 1 to 133 of SEQ ID 63 are nearly identical to nucleotides 862 to 994 of SEQ ID 63, resulting in amino acids 1 to 33 of SEQ ID NO: 186 being identical to amino acids 8 to 40 of SEQ ID NO: 187.

The restriction fragment obtainable from the deposit containing clone should be approximately 2113 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as R79825 sl Soares placenta Nb2HP Homo sapiens clone IMAGE: 3', sequence). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity. The computer program predicts a potential transmembrane domain within the protein sequence centered around amino acid 64 of SEQ ID 64. The nucleotide sequence of vo16_1 indicates that it may contain an Alu repeat region.

A polynucleotide of the present invention has been identified as vo18_1 was isolated from a human adult pancreas library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID 65, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence

of the vo 18_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 66. Amino acids 10 to 22 of SEQ ID 66 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23.

The restriction fragment obtainable from the deposit containing clone vo18_1 should be approximately 624 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as Homo sapiens clone IMAGE 1755025 3', sequence). Based upon sequence similarity, vo18_1 proteins and each similar protein or peptide may share at least some activity.

Clone"vol9 A polynucleotide of the present invention has been identified as vo19_1 was isolated from a human adult pancreas library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo19_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID 67, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo19_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 68. Amino acids 8 to 20 of SEQ ID 68 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21.

The restriction fragment obtainable from the deposit containing clone should be approximately 1957 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as Homo sapiens clone IMAGE: 2117032 3', sequence) and V42646 (DNA encoding a human pathogenesis-related protein designated HPRP). The predicted amino acid sequence disclosed herein for was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted protein demonstrated at least some similarity to sequences identified as (glioma pathogenesis-related protein [Homo sapiens] and W63115 (A human pathogenesis-related protein designated HPRP). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity.

Clone"vo22 1" A polynucleotide of the present invention has been identified as was isolated from a human adult pancreas library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as"vo22_1 protein").

The nucleotide sequence as presently determined is reported in SEQ ID 69, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 70. Amino acids 6 to 18 of SEQ ID 70 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19.

If one of the"G"nucleotides at positions 385 and 386 of SEQ ID 69 were deleted, and the"G"residue at position 312 of SEQ ID 69 changed to a"T", another potential reading frame and predicted amino acid sequence, encoded by what would then be basepairs 104 to 430 of SEQ ID 69, is reported in SEQ ID

Amino acids 8 to 20, amino acids 7 to 19, amino acids 6 and amino acids 9 to 21 of SEQ ID 188 are predicted leader/signal sequences, with the predicted mature amino acid sequence beginning at amino acid 21, or at amino acid 20, or at amino acid or at amino acid 22, respectively. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO: 188.

Another potential reading frame and predicted amino acid sequence, encoded by basepairs 1150 to 1357 of SEQ ID 69, is reported in SEQ ID

Amino acids 3 to 15 of SEQ ID 189 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 16. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID 189.

The restriction fragment obtainable from the deposit containing clone should be approximately 2091 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AA706247 parathyroid tumor Homo sapiens clone 1240148 3', sequence) and V34194 (Human secreted protein gene 41 clone The predicted amino acid sequence disclosed herein for was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted protein demonstrated at least some similarity to sequences identified as AF01644 (No definition line found [Caenorhabditis elegans]) and W75155 (Human secreted protein encoded by gene 41 clone HNTME13).

Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity. The computer program predicts 9 potential transmembrane domains within the protein sequence, centered around amino acids 50,120,165,250,275,309,356,374, and 392 of SEQ ID 70, respectively.

Clone"vo23 1" A polynucleotide of the present invention has been identified as was isolated from a human adult pancreas library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 72.

The restriction fragment obtainable from the deposit containing clone should be approximately 2598 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo23_1 demonstrated at least some similarity with sequences identified as T23658 (Human gene signature HUMGS05523), W81246 (zd85b01. rl Soares fetal heart NbHH19W Homo sapiens clone 347401 sequence), and Z84488 (Human DNA sequence from PAC 93H18 on chromosome 6 contains ESTs heterochromatin protein HP1Hs-gamma pseudogene, STS and CpG island). Based upon sequence similarity, vo23_1 proteins and each similar protein or peptide may share at least some activity. The computer program predicts two potential transmembrane domains within the protein sequence, one

centered around amino acid 428 and another around amino acid 472 of SEQ ID 72.

Clone"vo24 A polynucleotide of the present invention has been identified as was isolated from a human adult pancreas library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo24_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID 73, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 74. Amino acids 10 to 22 of SEQ ID 74 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23.

The restriction fragment obtainable from the deposit containing clone should be approximately 3484 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AC003117 (*** SEQUENCING IN PROGRESS *** Human chromosome 1 BAC 308G1 genomic sequence; HTGS phase unordered pieces), V10696 (Human 3.5 kB DNA fragment predicted to contain gene), and Z94054 (Human DNA sequence from PAC 125H23 on chromosome The predicted amino acid sequence disclosed herein for was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted protein demonstrated at least some similarity to sequences identified as W58774 (Human breast cancer gene protein fragment #1). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence indicates that it may contain one or more of the following repetitive elements: Alu, Mer33.

Clone"vo25 A polynucleotide of the present invention has been identified as was isolated from a human adult pancreas library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo25_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID 75, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo25_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 76. Amino acids 11 to 23 of SEQ ID 76 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24.

The restriction fragment obtainable from the deposit containing clone should be approximately 1200 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as xl Homo sapiens clone IMAGE 1902232 3'similar to WP CE01190;, sequence), V34218 (Human secreted protein gene 65 clone HSREG44), and Z55702 (H. sapiens CpG island DNA genomic Msel fragment, clone forward read The predicted amino acid sequence disclosed herein for vo25_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted protein demonstrated at least some similarity to sequences identified as U21324 (similar to S. cerevisiae hypothetical protein [Caenorhabditis elegans]) and W57893 (Protein of clone Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity. Motifs analysis detected an ATP/GTP-

binding site motif A (P-loop) centered around residue 229 of SEQ ID 76. The computer program predicts a potential transmembrane domain within the protein sequence centered around amino acid 170 of SEQ ID NO: 76.

Clone"vo26 A polynucleotide of the present invention has been identified as was isolated from a human adult pancreas library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo26_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID 77, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 78. Amino acids 13 to 25 of SEQ ID 78 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26.

The restriction fragment obtainable from the deposit containing clone should be approximately 2503 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AC004707 (Homo sapiens chromosome 17, clone complete sequence), sapiens clone IMAGE 1709042 3'similarto P12687 MITOCHONDRIAL 60S PROTEIN L2 PRECURSOR; sequence), and T23473 (Human gene signature HUMGS05312). The predicted amino acid sequence disclosed herein for was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted protein demonstrated at least some similarity to sequences identified as L37877 protein L27 [Filobasidiella Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence indicates that it may contain a Mir repeat.

A polynucleotide of the present invention has been identified as vp23_1 was isolated from a human adult prostate library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp23_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID 79, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp23_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 80. Amino acids 5 to 17 of SEQ ID 80 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

The restriction fragment obtainable from the deposit containing clone vp23_1 should be approximately 1220 bp.

The nucleotide sequence disclosed herein for vp23_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using and FASTA search protocols. vp23_1 demonstrated at least some similarity with sequences identified as AL021578 (Human DNA sequence from clone 453C12 on chromosome Contains SDC4 (syndecan 4 ryudocan)), predicts a gene like the mouse transcription factor RBP-L). Based upon sequence similarity, vp23_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence indicates that it may contain an Alu repetitive element.

A polynucleotide of the present invention has been identified as was isolated from a human adult lung library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq7_l is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 82. Amino acids 9 to 21 of SEQ ID 82 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone should be approximately 1326 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AA036918 rl Soares pregnant uterus Homo sapiens clone 484540 5', sequence). The predicted amino acid sequence disclosed herein for was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq7_l protein demonstrated at least some similarity to sequences identified as (butyrophilin-like protein [Mus musculus]). Butyrophilin is a glycoprotein of the immunoglobulin superfamily that is secreted in association with the milk-fat-globule membrane from mammary epithelial cells (Ogg et al., 1996, Mamm. Genome 7 (12): 900-905, which is incorporated by reference herein). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence indicates that it may contain a repetitive element.

Clone"vq8 1" A polynucleotide of the present invention has been identified as was isolated from a human adult lung library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID 83, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 84. Amino acids 10 to 22 of SEQ ID 84 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

The restriction fragment obtainable from the deposit containing clone should be approximately 695 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AA433968 rl Soares ovary tumor NbHOT Homo sapiens clone 770149 5', sequence) and V69618 (Human secreted protein gene 8 clone HLHCM89). The predicted amino acid sequence disclosed herein for was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted protein demonstrated at least some similarity to sequences identified as W83953 (Polypeptide encoded by gene 7 clone

HJPDJ64). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity.

A polynucleotide of the present invention has been identified as was isolated from a human adult lung library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence of vq9_1 as presently determined is reported in SEQ ID 85, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq9_l protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 86. Amino acids 5 to 17 of SEQ ID 86 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

The restriction fragment obtainable from the deposit containing clone should be approximately 1218 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AA769310 Homo sapiens clone IMAGE: 1290173, sequence). The predicted amino acid sequence disclosed herein for vq9_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted protein demonstrated at least some similarity to sequences identified as U79260 (unknown [Homo sapiens]) and W48351 (Human breast cancer related protein BCRB2). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity.

Clone"vqlO 1" A polynucleotide of the present invention has been identified as clone"vql0_l". was isolated from a human adult lung library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as"vql0_l protein").

The nucleotide sequence as presently determined is reported in SEQ ID 87, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 88. Amino acids 6 to 18 of SEQ ID are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

Another potential reading frame, encoded by nucleotides 331 to 834 of SEQ ID 87, is reported as the amino acid sequence of SEQ ID NO: 190. Amino acids 29 to 41 of SEQ ID 190 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 42. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO: 190.

If one nucleotide was deleted from the group of nucleotides at positions 330 and of SEQ ID 87, another potential reading frame would be created from what would then be nucleotides 18 to 836, with a

predicted amino acid sequence reported as SEQ ID NO: 191. Amino acids 6 to 18 of SEQ ID NO: 191 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:

The restriction fragment obtainable from the deposit containing clone should be approximately 1516 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AA359702 (EST68843 Fetal lung II Homo sapiens 5'end similar to similar to pulmonary surfactant protein B, sequence), I08571 (Sequence 14 from Patent WO 8706588), and Q79287 (Human pulmonary surfactant protein B (SPB)). The predicted amino acid sequence disclosed herein for was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq protein demonstrated at least some similarity to sequences identified as J02761 (pulmonary surfactant-associated protein SP-B [Homo sapiens]) and P70664 (6kd pulmonary surfactant protein). Pulmonary surfactant associated proteins such as SP- B promote alveolar stability by lowering the surface tension at the air-liquid interface in the peripheral air spaces. Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of indicates that it may contain an Alu repetitive element.

A polynucleotide of the present invention has been identified as was isolated from a human adult lung library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID 89, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 90. Amino acids 10 to 22 of SEQ ID 90 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

The restriction fragment obtainable from the deposit containing clone should be approximately 2284 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AA928678 Homo sapiens clone IMAGE 1559940 3', sequence), AB023187 (Homo sapiens for KIAA0970 protein, complete cds), and T19039 (Human gene signature HUMGS00046). Based upon sequence similarity, vq proteins and each similar protein or peptide may share at least some activity.

Clone"vq 16 A polynucleotide of the present invention has been identified as was isolated from a human adult lung library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID and includes a poly (A) tail.

What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 92. Amino acids 34 to 46 of SEQ ID 92 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 47. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone should be approximately 1087 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AA400700 Homo sapiens clone IMAGE: 5'similar to WP: R05D3.2 sequence). The predicted amino acid sequence disclosed herein for was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq16_1 protein demonstrated at least some similarity to sequences identified as (unknown Based upon sequence similarity, vq16_1 proteins and each similar protein or peptide may share at least some activity. The computer program predicts three additional potential transmembrane domains within the protein sequence, centered around amino acids 90,134, and 174 of SEQ ID 92, respectively.

19 A polynucleotide of the present invention has been identified as was isolated from a human adult lung library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq19_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID 93, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 94. Amino acids 11 to 23 of SEQ ID 94 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq19_1 protein.

The restriction fragment obtainable from the deposit containing clone vq19_1 should be approximately bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AA577696 Homo sapiens clone IMAGE: 1084661 3'similar to contains Alu repetitive element; sequence. Based upon sequence similarity, vq19_1 proteins and each similar protein or peptide may share at least some activity. The computer program predicts an additional potential transmembrane domains within the protein sequence centered around amino acid 214 of SEQ ID 94. The nucleotide sequence of indicates that it may contain an Alu repetitive element.

A polynucleotide of the present invention has been identified as vq20_1 was isolated from a human adult lung library and was identified as encoding secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq20_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence of vq20_1 as presently determined is reported in SEQ ID 95, and includes a

poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 96. Amino acids 10 to 22 of SEQ ID 96 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

The restriction fragment obtainable from the deposit containing clone should be approximately 1275 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AA826249 Homo sapiens clone IMAGE 1420806 3'similar to TR Q13445 Q13445 PUTATIVE T1/ST2 RECEPTOR BINDING PROTEIN PRECURSOR; sequence), pregnant uterus Homo sapiens clone IMAGE: 1712997 3'similar to TR: Q13445 Q13445 PUTATIVE RECEPTOR BINDING PROTEIN PRECURSOR; sequence), U41805 (Mus musculus putative receptor binding protein precursor partial cds), and V17729 (Human receptor-like ligand II cDNA). The predicted amino acid sequence disclosed herein for was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq20_1 protein demonstrated at least some similarity to sequences identified as U41804 (putative T1/ST2 receptor binding protein precursor [Homo sapiens]) and W48335 (Human Tl receptor-like ligand T1/ST2 is a receptor-like molecule homologous to the type I interleukin-1 receptor (Gayle et 1996, J. Chem. 271 5784-5789, which is incorporated by reference herein).

Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity. The computer program predicts an additional potential transmembrane domain within the vq20_1 protein sequence centered around amino acid 208 of SEQ ID 96.

A polynucleotide of the present invention has been identified as vq21_1 was isolated from a human adult lung library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID 97, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq21_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 98. Amino acids 16 to 28 of SEQ ID 98 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 29. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

The restriction fragment obtainable from the deposit containing clone should be approximately 1230 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as Stratagene colon (#937204) Homo sapiens clone IMAGE 566456 3'similar to contains Alu repetitive element; sequence), AC005282 (Homo sapiens clone WORKING DRAFT SEQUENCE, 4 unordered pieces), T25413 (Human gene signature HUMGS07579). The predicted amino acid sequence disclosed herein for vq21_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted protein demonstrated at least some similarity to sequences identified as U67577 (cell division

protein FtsJ [Methanococcus jannaschii]). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity.

Clone"vr2 1" A polynucleotide of the present invention has been identified as was isolated from a human adult lung library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence of as presently determined is reported in SEQ ID 99. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO: 100.

The restriction fragment obtainable from the deposit containing clone should be approximately 1382 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant similarities were identified in the databases. The computer program predicts a potential transmembrane domain within the protein sequence centered around amino acid 85 of SEQ ID 100. The nucleotide sequence of indicates that it may contain one ore more of the following repetitive elements: Alu, MER2, MER4B.

Clone"vc69 1" A polynucleotide of the present invention has been identified as was isolated from a human fetal brain library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID NO: 101, and includes (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO: 102. Amino acids 7 to 19 of SEQ ID 102 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone should be approximately 1600 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AB023138 (Homo sapiens for KIAA0921 protein, partial cds), and (tf45c01. xl Homo sapiens clone IMAGE 2099136 3'similar to TR Q63376 Q63376 PRECURSOR; sequence). The predicted amino acid sequence disclosed herein for was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted protein demonstrated at least some similarity to sequences identified as AB02313 (KIAA0921 protein [Homo sapiens]), and various isoforms of Rattus norvegicus neurexin II protein. Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity.

1" A polynucleotide of the present invention has been identified as was isolated from a human fetal brain library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc71_1 is a full-length clone,

including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in NO: 103, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc71_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO: 104. Amino acids 2 to 14 of SEQ ID 104 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone should be approximately bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as xl Soares_NhHMPu_Sl Homo sapiens clone IMAGE 2113663 3', sequence) and AL050018 (Homo sapiens proteins and each similar protein or peptide may share at least some activity.

Clone"vo27 1" A polynucleotide of the present invention has been identified as was isolated from a human adult pancreas library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as"vo27_1 protein").

The nucleotide sequence as presently determined is reported in SEQ ID NO: 105, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID 106. Amino acids 13 to 25 of SEQ ID 106 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

Another potential reading frame, encoded by nucleotides 1665 to 1844 of SEQ ID NO: 105, is reported as the amino acid sequence of SEQ ID NO: 192. Amino acids 4 to 16 of SEQ ID 192 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 17; amino acids 28 to 40 of SEQ ID NO: 192 are also a possible leader/signal sequence, with the predicted mature amino acid sequence beginning in that case at amino acid Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the protein of SEQ ID NO: 192.

The restriction fragment obtainable from the deposit containing clone should be approximately 2433 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AC007621 (Homo sapiens clone DRAFT SEQUENCE, 142 unordered pieces), (ao89gl xl Schiller meningioma Homo sapiens clone IMAGE 1953092 3'similar to contains Alu repetitive element; sequence), and X80059 (Human nucleotide sequence). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the protein sequence centered around amino acid 400 of SEQ ID 106. The nucleotide sequence of

indicates that it may contain an Alu repetitive element.

A polynucleotide of the present invention has been identified as was isolated from a human adult pancreas library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence of vo31_1 as presently determined is reported in SEQ ID 107, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo31_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO: 108. Amino acids 7 to 19 of SEQ ID 108 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

Another potential reading frame, encoded by nucleotides 1937 to 3007 of SEQ ID 107, is reported as the amino acid sequence of SEQ ID 193.

The restriction fragment obtainable from the deposit containing clone should be approximately 3222 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AF022147 (Rattus norvegicus uterus-ovary specific putative transmembrane protein (uo) complete cds), Homo sapiens clone IMAGE 2115096 3'similar to TR 035360 035360 UTERUS- OVARY SPECIFIC PUTATIVE TRANSMEMBRANE PROTEIN; mRNA sequence), (Protein clone DNA35841-1173). The predicted amino acid sequence disclosed herein for was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo31_1 protein demonstrated at least some similarity to sequences identified as AF02214 (uterus-ovary specific putative transmembrane protein [Rattus norvegicus]) and Y13377 (Amino acid sequence of protein Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity. The computer program predicts a potential transmembrane domain within the protein sequence of SEQ ID NO: 193, centered around amino acid 328 of SEQ ID NO: 193.

Hidden markov model analysis indicates the presence of Zona-pellucida-like domains at amino acids 26-115 and 146-273 of SEQ ID NO: 193. The nucleotide sequence of indicates that it may contain a Mer5a repetitive element.

Clone"vo32 1" A polynucleotide of the present invention has been identified as was isolated from a human adult pancreas library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID NO: 109, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO: 110. Amino acids 4 to 16 of SEQ ID 110 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 17. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

The restriction fragment obtainable from the deposit containing clone should be approximately 1868 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AF028740 (Mus musculus olfactomedin complete cds), Homo sapiens clone IMAGE 1676819 3'similar to TR Q99784 Q99784 NEURONAL OLFACTOMEDIN-RELATED ER LOCALIZED PROTEIN; sequence), AI869993 xl NCI_CGAP Brn25 Homo sapiens clone IMAGE: 2429608 3'similar to SW: NOMR_HUMAN Q99784 NEURONAL OLFACTOMEDIN-RELATED ER LOCALIZED PROTEIN; mRNA sequence), and V34217 (Human secreted protein gene 64 clone HSLDJ95). The predicted amino acid sequence disclosed herein for was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol.

The predicted protein demonstrated at least some similarity to sequences identified as U03416 (neuronal olfactomedin-related ER localized protein [Rattus norvegicus]) and W75120 (Human secreted protein encoded by gene 64 clone HSLDJ95). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity.

Clone"vo33 A polynucleotide of the present invention has been identified as was isolated from a human adult pancreas library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID NO: 111, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO: 112. Amino acids 5 to 17 of SEQ ID 112 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

The restriction fragment obtainable from the deposit containing clone should be approximately 2879 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as Sugano mouse kidney mkia Mus musculus clone IMAGE: 1907928 5'similar to TR: INHIBITOR FAMILY HEAVY CHAIN-RELATED PROTEIN; mRNA sequence) and X80054 (Human nucleotide sequence). The predicted amino acid sequence disclosed herein for was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted protein demonstrated at least some similarity to sequences identified as D38535 (PK-120 precursor [Homo sapiens]), Y 11545 heavy-chain H2 [Sus scrofa]), and the H2 proteins of several species, including Homo sapiens. Based upon sequence similarity, computer program predicts a potential transmembrane domain within the protein sequence centered around amino acid 386 of SEQ ID 112. The nucleotide sequence indicates that it may contain an Alu repetitive element.

A polynucleotide of the present invention has been identified as was isolated from a human adult lung library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID NO: 113, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO: 114. Amino acids 18 to 30 of SEQ ID 114 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

Another potential reading frame, encoded by nucleotides to 1518 of SEQ ID NO: 113, is reported as the amino acid sequence of SEQ ID NO: 194. Amino acids 83 to 94 of SEQ ID 194 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 95. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of protein of SEQ ID 194.

The restriction fragment obtainable from the deposit containing clone should be approximately 1793 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AA625521 rl Soares_NhHMPu_Sl Homo sapiens clone IMAGE 1047579 5', sequence) and AC002364 (Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vq23_1 indicates that it may contain an Alu repetitive element.

Clone"vq24 1" A polynucleotide of the present invention has been identified as was isolated from a human adult lung library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID NO: 115, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq24_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO: 116. Amino acids 5 to 17 of SEQ ID 116 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

The restriction fragment obtainable from the deposit containing clone should be approximately 2168 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as N29315 rl Soares melanocyte 2NbHM Homo sapiens clone IMAGE: 264491 5'similar to SP: SW: P12315 HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR I'B FORM'PRECURSOR; mRNA sequence). The predicted amino acid sequence disclosed herein for was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted protein demonstrated at least some similarity to sequences identified as (high affinity immunoglobulin gamma Fc receptor I [Mus musculus]) and R12428 (Hybrid Fc (gamma) RII/I receptor). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity. Hidden markov model analysis

detects immunoglobulin superfamily signatures in the vq24_1 protein sequence from amino acid 92 to amino acid 145, and from amino acid 185 to amino acid 242, of SEQ ID 116. The nucleotide sequence of indicates that it may contain one or more of the following repetitive elements: Mer,

Clone"vq261" A polynucleotide of the present invention has been identified as was isolated from a human adult lung library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein protein").

The nucleotide sequence as presently determined is reported in SEQ ID NO: 117, and includes a poly (A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO: 118. Amino acids 9 to 21 of SEQ ID 118 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein.

The restriction fragment obtainable from the deposit containing clone should be approximately 1419 bp.

The nucleotide sequence disclosed herein for was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. demonstrated at least some similarity with sequences identified as AA191552 s 1 Stratagene HeLa cell s3 937216 Homo sapiens clone IMAGE 626742 3', sequence) and AA573741 s 1 NCI_CGAP_Co2 Homo sapiens clone IMAGE: 1012784 3', sequence). Based upon sequence similarity, proteins and each similar protein or peptide may share at least some activity.

of Clones Clones were deposited on February 17,1999 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U. S. A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 207114, from which each clone comprising a particular polynucleotide is obtainable.

Clone was deposited on February 17,1999 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U. S. A.) as an original deposit under the Budapest Treaty and was given the accession number ATCC 207115, from which the clone comprising a particular polynucleotide is obtainable.

Clones vb28_1,vb29_1,vb30_1,vc67_1,vf4_1,vg3_1,vo2_1,vb27_1, vo5_1, vo6_1, and vo9_1 were deposited on July 15,1999 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U. S. A.) as an original deposit under the Budapest Treaty and were given the accession number PTA-362, from which each clone comprising a particular polynucleotide is obtainable.

Clones voll_l, vo22_1, vo25_1,andvo26_1weredepositedonJuly15,1999withthevo24_1, ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U. S. A.) as an original deposit under the Budapest Treaty and were given the accession number PTA-366, from which each clone comprising a particular polynucleotide is obtainable.

Clones vp23_1, vq9_1, vql6_l, vq21_l, and were deposited on July 15,1999 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U. S. A.) as an original deposit under the Budapest Treaty and were given the accession number PTA-368, from which

each clone comprising a particular polynucleotide is obtainable.

Clones and were deposited on December 21,1999 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U. S. A.) as an original deposit under the Budapest Treaty and were given the accession number PTA-1075, from which each clone comprising a particular polynucleotide is obtainable.

All restrictions on the availability to the public of the deposited material will be irrevocably removed upon the granting of the patent, except for the requirements specified in 37 C. F. R. § 1.808 (b), and the term of the deposit will comply with 37 C. F. R. § 1.806.

Each clone has been transfected into separate bacterial cells (E. coli) in these composite deposits. Each clone can be removed from the vector in which it was deposited by an digestion (5'site, EcoRI; 3'site, NotI) to produce the appropriate fragment for such clone. Each clone was deposited in either the pED6 or pNOTs vector depicted in Figures and 1B, respectively. The pED6dpc2 vector ("pED6") was derived from by insertion of a new polylinker to facilitate deletion of the DHFR sequences, insertion of a new polylinker, and insertion of the origin of replication in the ClaI site. In some instances, the deposited clone can become "flipped" (i. e., in the reverse orientation) in the deposited isolate. In such instances, the insert can still be isolated by digestion with EcoRI and NotI. However, NotI will then produce the 5'site and EcoRI will produce the 3'site for placement of the in proper orientation for expression in a suitable vector. The may also be expressed from the vectors in which they were deposited.

Bacterial cells containing a particular clone can be obtained from the composite deposit as follows: An oligonucleotide probe or probes should be designed to the sequence that is known for that particular clone. This sequence can be derived from the sequences provided herein, or from a combination of those sequences. The sequence of an oligonucleotide probe that was used to isolate or to sequence each full-length clone is identified below, and should be most reliable in isolating the clone of interest.

IDNO:121vp11_1SEQ vpl3_lSEQIDNO: 122 IDNO:128vq5_1SEQ IDNO:130vr1_1SEQ IDNO:131vc63_1SEQ IDNO:135vb29_1SEQ IDNO:137vc67_1SEQ IDNO:138vf4_1SEQ IDNO:139vg3_1SEQ IDNO:140vo2_1SEQ IDNO:141vo3_1SEQ IDNO:142vo5_1SEQ IDNO:144vo9_1SEQ IDNO:145vo11-1SEQ IDNO:147vo13_1SEQ vol4_lSEQIDNO: 148 vol5_lSEQIDNO: 149 vol8_1 SEQ ID NO : 151 vol9_1 SEQ ID NO : 152 vo22_1 SEQ ID NO : 153 vo23_1 SEQ ID NO : 154 vo24_1 SEQ ID NO : 155 vo26_1 SEQ ID NO : 157 vq7_1 SEQ ID NO : 159 vq8_1 SEQ ID NO : 160 vq9_1 SEQ ID NO : 161 SEQ ID NO : 162 vql3_1 SEQ ID NO : 163 vql6_1 SEQ ID NO : 164 vql9_1 SEQ ID NO : 165 vq20_1 SEQ ID NO : 166 vq21_1 SEQ ID NO : 167 IDNO:168vr2_1SEQ In the sequences listed above which include an N at position 2, that position is occupied in preferred probes/primers by a biotinylated phosphoaramidite residue rather than a nucleotide (such as, for example, that produced by use of biotin phosphoramidite (1- (N-biotinyl-4-aminobutyl)-propyl-3-0-(2-cyanoethyl)-(N,(N-biotinyl-4-aminobutyl)-propyl-3-0-(2-cyanoethyl)-(N, N- diisopropyl)-phosphoramadite) (Glen Research, cat. no. 10-1953)).

The design of the oligonucleotide probe should preferably follow these parameters: (a) It should be designed to an area of the sequence which has the fewest ambiguous bases ("N's"), if any; (b) It should be designed to have a of approx. 80 (assuming each A or T and 4 degrees for each G or C). Ci/mmole) and T4 polynucleotide kinase using commonly employed techniques for labeling oligonucleotides. Other labeling techniques can also be used. Unincorporated label should preferably be removed by gel filtration chromatography or other established methods. The amount of radioactivity incorporated into the probe should be quantitated by measurement in a scintillation counter. Preferably, specific activity of the resulting probe should be approximately 4e+6 dpm/pmole.

The bacterial culture containing the pool of full-length clones should preferably be thawed and of the stock used to inoculate a sterile culture flask containing 25 ml of sterile L-broth containing ampicillin at 100 The culture should preferably be grown to saturation at and the saturated culture should preferably be diluted in fresh L-broth. Aliquots of these dilutions should preferably be plated to determine the dilution and volume which will yield approximately 5000 distinct and well-separated colonies on solid bacteriological media containing L-broth containing at 100 and agar at 1.5% in a 150 mm petri dish when grown overnight at Other known methods of obtaining distinct, well-separated colonies can also be employed.

Standard colony hybridization procedures should then be used to transfer the colonies to nitrocellulose filters and lyse, denature and bake them.

The filter is then preferably incubated at 65 C for 1 hour with gentle agitation in 6X SSC (20X stock is 175.3 g 88.2 g Na citrate/liter, adjusted to pH 7.0 with containing 0.5% SDS, of yeast RNA, and 10 mM EDTA (approximately 10 mL per 150 mm filter). Preferably, the probe is then added to the hybridization mix at a concentration greater than or equal to dpm/mL. The filter is then preferably incubated at 65 C with gentle agitation overnight. The filter is then preferably washed in 500 mL of 2X SSC/0.5% SDS at room temperature without agitation, preferably followed by 500 mL of 2X SSC/0.1% SDS at room temperature with gentle shaking for 15 minutes. A third wash with SSC/0.5% SDS at 65°C for 30 minutes to 1 hour is optional. The filter is then preferably dried and subjected to autoradiography for sufficient time to visualize the positives on the X-ray film. Other known hybridization methods can also be employed.

The positive colonies are picked, grown in culture, and plasmid DNA isolated using standard procedures. The clones can then be verified by restriction analysis, hybridization analysis, or DNA sequencing.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, incorporated herein by reference. Such fragments may be fused to carrier molecules such as for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through"linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein-IgM fusion would generate a decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form (s) of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with the ATCC) in a suitable mammalian cell or other host cell. The sequence (s) of the mature form (s) of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein."Corresponding genes"are the regions of the genome that are transcribed to produce the mRNAs from which polynucleotide sequences are derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5'and regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification

amplification of genes in appropriate genomic libraries or other sources of genomic materials. An"isolated gene"is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

The chromosomal location corresponding to the polynucleotide sequences disclosed herein may also be determined, for example by hybridizing appropriately labeled polynucleotides of the present invention to chromosomes in situ. It may also be possible to determine the corresponding chromosomal location for a disclosed polynucleotide by identifying significantly similar nucleotide sequences in public databases, such as expressed sequence tags (ESTs), that have already been mapped to particular chromosomal locations. For at least some of the polynucleotide sequences disclosed herein, public database sequences having at least some similarity to the polynucleotide of the present invention have been listed by database accession number. Searches using the GenBank accession numbers of these public database sequences can then be performed at an Internet site provided by the National Center for Biotechnology Information having the address http://www. ncbi. nlm. nih. gov/UniGene/, in order to identify"UniGene clusters"of overlapping sequences. Many of the"UniGene clusters"so identified will already have been mapped to particular chromosomal sites.

Organisms that have enhanced, reduced, or modified expression of the gene (s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind cleave the transcribed from the gene (Albert and Morris, 1994, Trends Sci. 15 (7): 250-254; Lavarosky et al., 1997, Biochem.

Mol. Med. 62 11-22; 1998, Prog. 58: 1-39; all of which are incorporated by reference herein). The desired change in gene expression can also be achieved through the use of double-stranded ribonucleotide molecules having some complementarity to the transcribed from the gene, and which interfere with the transcription, stability, or expression of the ("RNA 1998, Nature 391 (6669): 806-811; 1998, Proc. Natl. Acad.

Sci. (26): 15502-15507; 13 (2): all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene (s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 incorporated by reference herein). In addition, organisms are provided in which the gene (s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene (s) or through deletion of all or part of the corresponding gene (s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, Bioessays 14 (9): 629-633; Zwaal et al., 1993, Proc. Natl. Acad. Sci. USA 90 (16): 7431-7435; Clark et al., 1994, Proc. Natl. Acad. Sci. USA 91 (2): 719-722; all of which are incorporated by reference herein), or through homologous recombination, preferably detected by positive/negative genetic selection strategies (Mansour et 1988, Nature 336: 348-352; U. S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614,396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene (s), and for the development of assay systems for the identification of molecules that interact with the protein product (s) of the corresponding gene (s).

Where the protein of the present invention is membrane-bound (e. g., is the present invention also provides for soluble forms of such protein. In such forms, part or all of the intracellular and

transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information. For example, the computer program can be used to predict the location of transmembrane domains in an amino acid sequence, domains which are described by the location of the center of the transmsmbrane domain, with at least ten transmembrane amino acids on each side of the reported central residue (s).

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

In particular, sequence identity may be determined using WU-BLAST (Washington University BLAST) version 2.0 software, which builds upon WU-BLAST version 1.4, which in turn is based on the public domain NCBI-BLAST version 1.4 (Altschul and Gish, 1996, Local alignment statistics, Doolittle Methods in Enzymology 266: 460-480; Altschul 1990, Basic local alignment search tool, Journal ofMolecularBiology 215 : 403-410; Gish and States, 1993, Identification of protein coding regions by database similarity search, Nature 266-272; Karlin and Altschul, 1993, Applications and statistics for multiple high-scoring segments in molecular sequences, Proc. Natl. Acad. Sci.

USA 90: 5873-5877; all of which are incorporated by reference herein). WU-BLAST version 2.0 executable programs for several UNIX platforms can be downloaded from ftp://blast. wustl. edu/blast/executables. The complete suite of search programs (BLASTP, BLASTN, BLASTX, TBLASTN, and TBLASTX) is provided at that site, in addition to several support programs. WU-BLAST 2.0 is copyrighted and may not be sold or redistributed in any form or manner without the express written consent of the author; but the posted executables may otherwise be freely used for commercial, nonprofit, or academic purposes. In all search programs in the BLASTN, BLASTX, TBLASTN and TBLASTX--the gapped alignment routines are integral to the database search itself, and thus yield much better sensitivity and selectivity while producing the more easily interpreted output. Gapping can optionally be turned off in all of these programs, if desired. The default penalty (Q) for a gap of length one is Q=9 for proteins and BLASTP, and for BLASTN, but may be changed to any integer value including zero, one through eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. The default per-residue penalty for extending a gap (R) is R=2 for proteins and BLASTP, and for BLASTN, but may be changed to any integer value including zero, one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. Any combination of values for Q and R can be used in order to align sequences so as to maximize overlap and identity while minimizing sequence gaps. The default amino acid comparison matrix is BLOSUM62, but other amino acid comparison matrices such as PAM can be utilized.

Species homologues of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a"species homologue"is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide. Preferably, polynucleotide species homologues have at least 60%

sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, and protein species homologues have at least 30% sequence identity (more preferably, at least 45% identity; most preferably at least 60% identity) with the given protein, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides or the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Species homologues may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species. Preferably, species homologues are those isolated from mammalian species. Most preferably, species homologues are those isolated from certain mammalian species such as, for example, Pan troglodytes, Gorilla gorilla, Pongo pygmaeus, Hylobates concolor, Macaca mulatta, Papio papio, Papio hamadryas, Cercopithecus aethiops, Cebus capucinus, Aotus trivirgatus, Sanguinus oedipus, Microcebus murinus, Mus musculus, Rattus norvegicus, Cricetulus griseus, Felis catus, Mustela scrofa, and Equus caballus, for which genetic maps have been created allowing the identification of syntenic relationships between the genomic organization of genes in one species and the genomic organization of the related genes in another species (O'Brien and Seuanez, 1988, Ann. Rev. Genet. 22: 323-351; O'Brien et 1993, Nature 3: 103-112; Johansson et al., 1995, Genomics 25: 682-690; Lyons et 1997, Nature Genetics 15: 47-56; O'Brien et 1997, Trends in Genetics 13 (10): 393-399; Carver and Stubbs, 1997, Genome Research 7: 1123-1137; all of which are incorporated by reference herein).

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotides which also encode proteins which are identical or have significantly similar sequences to those encoded by the disclosed polynucleotides. Preferably, allelic variants have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. Allelic variants may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from individuals of the appropriate species.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides that hybridize under reduced stringency conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R. Stringency Polynucleotide Hybrid Hybridization Temperature and Wash Condition Hybrid Length Buffert Temperature and (bp)'Buffer A DNA: DNA 250 65°C; lxSSC-or-65°C; 0.3xSSC 42°C; 1xSSC, 50% formamide B DNA: DNA <50 T* ; IxSSC T ; IxSSC C DNA: RNA 2 50 67°C; lxSSC-or-67°C; 0.3xSSC 45°C; 1xSSC, 50% formamide D DNA: RNA <50 TD*; lxSSC TD*; IxSSC E RNA: RNA 250 70°C; lxSSC-or-70°C; 0.3xSSC 50°C; 1xSSC, 50% formamide F RNA: RNA <50 TF*; 1xSSC TF* ; IxSSC G DNA: DNA # 50 65°C ; 4xSSC-or-65° C; IxSSC 42°C; 4xSSC, 50% formamide H DNA: DNA <50 TH*; 4xSSC TH*; 4xSSC I DNA: RNA 2 50 67°C; 4xSSC-or-67°C; lxSSC 45°C; 4xSSC, 50% formamide J DNA : RNA <50 Tj*; 4xSSC T, *; 4xSSC K RNA: RNA 5 50 70°C; 4xSSC-or-67°C; lxSSC 50°C; 4xSSC, 50% formamide L RNA: RNA <50 TL*; 2xSSC TL*; 2xSSC M DNA: DNA 2 50 50°C; 4xSSC-or-50°C; 2xSSC 40°C; 6xSSC, 50% formamide N DNA: DNA <50 TN*; 6xSSC TN*; 6xSSC O DNA: RNA 2 50 55°C; 4xSSC-or-55°C; 2xSSC 42°C; 6xSSC, 50% formamide P DNA: RNA <50 Tp*; 6xSSC TP*; 6xSSC Q RNA: RNA 2 50 60°C; 4xSSC-or-60°C; 2xSSC 45°C; 6xSSC, 50% formamide R RNA: RNA <50 TR*; 4xSSC TR*; 4xSSC hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length

is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity. t: SSPE (lxSSPE is and 1.25mM EDTA, pH 7.4) can be substituted for SSC is and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete. less than the melting temperature of the hybrid, where is determined according to the following equations. For and 49 base pairs in length, Tm = 81.5 + 16.6 (log10[Na+]) + 0.41 (% G+C)- (600/N), where N is the number of bases in the hybrid, and is the concentration of sodium ions in the hybridization buffer for IxSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E. F. Fritsch, and T. Maniatis, 1989, Molecular Cloning : A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and 1995, F. M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

The isolated polynucleotide endcoing the protein of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman Nucleic Acids Res. 19,4485-4490 in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185,537-566 (1990). As defined herein"operably linked"means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include strains, Candida, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include Escherichia coli, Bacillus subtilis, Salmonella typhimurium, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for cell expression systems are commercially available in kit form from, e. g., Invitrogen, San Diego, California, U. S. A. (the kit), and such methods are well known in the art,

1555 (1987), incorporated herein As used herein, an insect cell capable of expressing a polynucleotide of the present invention is"transformed." The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i. e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, or Cibacrom blue 3GA one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLabs (Beverly, MA), Pharmacia (Piscataway, NJ) and Invitrogen Corporation (Carlsbad, CA), respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope.

One such epitope ("Flag") is commercially available from the Eastman Kodak Company (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, e. g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an"isolated protein." The protein of the invention may also be expressed as a product of transgenic animals, e. g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis.

Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e. g., U. S.

Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains

the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

USES AND BIOLOGICAL ACTIVITY The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction

Research Uses and Utilities The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to"subtract-out"known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a"gene chip"or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, those described in Gyuris et 1993, Cell 75: 791-803 and in Rossi et 1997, Proc. Natl. Acad. Sci. USA 94: 8405-8410, all of which are incorporated by reference herein) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction.

Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References

disclosing such methods include without limitation"Molecular Cloning: A Laboratory Manual", 2d Cold Spring Harbor Laboratory Press, Sambrook, J., E. F.

Fritsch and T. Maniatis eds., 1989, and"Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

Nutritional Uses Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, B9, BaF3, MC9/G, M+ M+), 2E8, RB5, DA1,123, T1165, HT2, CTLL2, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods: Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137: 3494-3500,1986; Bertagnolli et al., J. Immunol. 145: 1706-1712,1990; Bertagnolli et Cellular Immunology 133: 327-341,1991; Bertagnolli, et al., J. Immunol. 149: 3778-3783,1992; Bowman et al., J. Immunol. 152: 1756-1761,1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology.

J. E. e. a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Schreiber, R. D. In Current Protocols in Immunology. J. E. e. a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto.

1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e. a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173: 1205-1211,1991; Moreau et Nature 336: 690-692,1988; Proc. Natl. Acad. Sci. U. S. A. 80: 2931-2938, 1983; Measurement of mouse and human interleukin 6-Nordan, R. In Current Protocols in Immunology. J. E. e. a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; et al., Proc. Natl. Acad. Sci. U. S. A. 83: 1857-1861,1986; Measurement of human Interleukin Giannotti, S. C. and Turner, K. J.

In Current Protocols in Immunology. J. E. e. a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. Measurement of mouse and human Interleukin 9-Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. e. a. Coligan eds.

Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77: 6091-6095,1980; Weinberger et al., Eur. J. Immun.

11: 405-411,1981; Takai et al., J. Immunol. 137: 3494-3500,1986; Takai et al., J.

Immunol. 140: 508-512,1988.

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e. g., in regulating (up or down) growth and proliferation and/or B lymphocytes, as well as effecting the cytolytic activity cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e. g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i. e., in the treatment of cancer.

disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain- Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems.

Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to regulate immune responses in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both.

Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent.

Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from

immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e. g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand (s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form having an activity lymphocyte antigen (e. g., B7- 1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand (s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans.

Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the effects of fusion proteins in vivo as described in Lenschow et al., Science 257: 789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89: 11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function in vivo on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms.

Administration of reagents which block costimulation of T cells by disrupting receptor: ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen- specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy.

Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen- pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e. g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides.

For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen (s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e. g., a protein to thereby express MHC class I or MHC class II proteins on the cell surface.

Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity lymphocyte antigen (e. B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods: Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing Associates and (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et Proc.

Natl. Acad. Sci. USA 78: 2488-2492,1981; J. Immunol. 128: 1968-1974, 1982; Handa et al., J. Immunol. 135: 1564-1572,1985; Takai et al., J. Immunol.

137: 3494-3500,1986; Takai J. Immunol. 140: 508-512,1988; Proc.

Natl. Acad. Sci. USA 78: J. Immunol. 128: 1968-1974, 1982; Handa et al., J. Immunol. 135: 1564-1572,1985; Takai et al., J. Immunol.

137: 3494-3500,1986; J. Virology 61: 1992-1998; J. Immunol.

140: 508-512,1988; Bertagnolli et al., Cellular Immunology 133: 327-341,1991; Brown et al., J. Immunol. 153: 3079-3092,1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect include, without limitation, those described in: Maliszewski, J. Immunol. 144: 3028-3033,1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology.

J. E. e. a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M.

Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1- 3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol.

137: 3494-3500,1986; Takai et al., J. Immunol. 140: 508-512,1988; Bertagnolli et al., J.

Immunol. 149: 3778-3783,1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134: 536-544,1995; Inaba et Journal of Experimental Medicine 173: 549-559,1991; Macatonia et Journal of Immunology 154: 5071-5079,1995; Porgador et Journal of Experimental Medicine 182: 255-260, 1995; Nair et al., Journal of Virology 67: 4062-4069,1993; Huang et al., Science 264: 961-965,1994; Macatonia et al., Journal of Experimental Medicine 169: 1255-1264, 1989; Bhardwaj et Journal of Clinical Investigation 94: 797-807,1994; and Inaba et Journal of Experimental Medicine 172: 631-640,1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13: 795-808,1992; Gorczycaetal., Leukemia7: 659-670,1993; et Cancer Research 53: 1945-1951,1993; Itoh et Cell 66: 233-243,1991; Zacharchuk, Journal of Immunology 145: 4037-4045,1990; Zamai et al., Cytometry 14: 891-897,1993; International Journal of Oncology 1: 639-648,1992.

Assays for proteins that influence early steps of T-cell and development include, without limitation,

those described in: Antica et al., Blood 84: 111-117,1994; Fine 155: 111-122,1994; Blood 85: 2770-2778,1995; Toki et al., Proc. Nat. Acad Sci. USA 88: 7548-7551,1991.

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e. g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i. e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo- suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i. e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods: Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15: 141-151,1995; Keller et al., Molecular and Cellular Biology 13: 473-486,1993; McClanahan et Blood 81:2903-2915,1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89: 5907-5911,1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A.

In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et Experimental Hematology 22: 353-359,1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture

R. I. Freshney, et al. eds. Vol pp. Wiley-Liss, Inc.., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth A protein of the present invention also may have utility in compositions used for bone,

cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is formation. A protein of the present invention, which induces tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon-or ligament-forming cells, stimulate growth of tendon-or ligament-forming cells, induce differentiation of progenitors of tendon-or ligament-forming cells, or induce growth of cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i. e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue.

More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome.

Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods: Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. (bone, cartilage, tendon); International Patent Publication No. W095/05846 (nerve, neuronal); International Patent Publication No. (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by and Mertz, J. Invest.

Dermatol 71: 382-84 (1978).

Activin/Inhibin A protein of the present invention may also exhibit activin-or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-0 group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods: Assays for activin/inhibin activity include, without limitation, those described in: Vale et Endocrinology 91: 562-572,1972; Ling et Nature 321: 779-782,1986; Vale et Nature 321: 776-779,1986; Mason et al., Nature 318: 659-663,1985; Forage et al., Proc. Natl. Acad. Sci. USA 83: 3091-3095,1986.

Chemotactic/Chemokinetic A protein of the present invention may have chemotactic or chemokinetic

activity (e. act as a chemokine) for mammalian cells, including, for example, monocytes, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells.

Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods: Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95: 1370-1376,1995; Lindet al. APMIS 103: 140-146,1995; J. Immunol. 25: 1744-1748;

J. 152: 5860-5867,1994; Johnstonetal. J. of Immunol. 153: 1762-1768,1994.

Hemostatic and Thrombolytic Activity A protein of the invention may also exhibit hemostatic or thrombolytic activity.

As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e. g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods: Assay for hemostatic and thrombolytic activity include, without limitation, those J. Clin. 26: 131-140,1986; Thrombosis Res. 45: 413-419,1987; Humphrey et al., Fibrinolysis 5: 71-79 (1991); Schaub, Prostaglandins 35: 467-474,1988.

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction.

A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods: Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H.

Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84: 6864-6868,1987; J. Exp. Med. 1145-1156,1988; Rosenstein J. Exp. Med.

169: 149-160 1989; Stoltenborgetal., J. Immunol. Methods 175: 59-68,1994; Cell 80: 661-670,1995.

Proteins of the present invention may also exhibit anti-inflammatory activity. The activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Cadherins are calcium-dependent adhesion molecules that appear to play major roles during development, particularly in defining specific cell types. Loss or alteration of normal cadherin expression can lead to changes in cell adhesion properties linked to tumor growth and metastasis. Cadherin malfunction is also implicated in other human diseases, such as pemphigus and pemphigus foliaceus (auto-immune blistering skin diseases), Crohn's disease, and some developmental abnormalities.

The cadherin superfamily includes well over forty members, each with a distinct pattern of expression. All members of the superfamily have in common conserved extracellular repeats (cadherin domains), but structural differences are found in other parts of the molecule. The cadherin domains bind calcium to form their tertiary structure and thus calcium is required to mediate their adhesion. Only a few amino acids in the first cadherin domain provide the basis for homophilic adhesion; modification of this recognition site can change the specificity of a cadherin so that instead of recognizing only itself, the mutant molecule can now also bind to a different cadherin. In addition, some cadherins engage in heterophilic adhesion with other cadherins.

E-cadherin, one member of the cadherin superfamily, is expressed in epithelial cell types.

Pathologically, if E-cadherin expression is lost in a tumor, the malignant cells become invasive and the cancer metastasizes. Transfection of cancer cell lines with polynucleotides expressing E- cadherin has reversed cancer-associated changes by returning altered cell shapes to normal, restoring cells'adhesiveness to each other and to their substrate, decreasing the cell growth rate, and drastically reducing anchorage-independent cell growth. Thus, reintroducing E-cadherin expression reverts

carcinomas to a less advanced stage. It is likely that other cadherins have the same invasion suppressor role in derived from other tissue types. Therefore, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to treat cancer. Introducing such proteins or polynucleotides into cancer cells can reduce or eliminate the cancerous changes observed in these cells by providing normal cadherin expression.

Cancer cells have also been shown to express cadherins of a different tissue type than their origin, thus allowing these cells to invade and metastasize in a different tissue in the body.

Proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be substituted in these cells for the inappropriately expressed cadherins, restoring normal cell adhesive properties and reducing or eliminating the tendency of the cells to metastasize.

Additionally, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can used to generate antibodies recognizing and binding to cadherins. Such antibodies can be used to block the adhesion of inappropriately expressed tumor-cell cadherins, preventing the cells from forming a tumor elsewhere. Such an anti-cadherin antibody can also be used as a marker for the grade, pathological type, and prognosis of a cancer, i. e. the more progressed the cancer, the less cadherin expression there will be, and this decrease in cadherin expression can be detected by the use of a cadherin-binding antibody.

Fragments of proteins of the present invention with cadherin activity, preferably a polypeptide comprising a decapeptide of the cadherin recognition site, and poly-nucleotides of the present invention encoding such protein fragments, can also be used to block cadherin function by binding to cadherins and preventing them from binding in ways that produce undesirable effects. Additionally, fragments of proteins of the present invention with cadherin activity, preferably truncated soluble cadherin fragments which have been found to be stable in the circulation of cancer patients, and polynucleotides encoding such protein fragments, can be used to disturb proper cell-cell adhesion.

Assays for cadherin adhesive and invasive suppressor activity include, without limitation, those described in: Hortsch et al. J Biol Chem 270 (32): 18809-18817,1995; Miyaki et al.

Oncogene 11: 2547-2552,1995; Ozawa et al. Cell 63: 1033-1038,1990.

Tumor Inhibition Activitv In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities.

A protein may inhibit tumor growth directly or indirectly (such as, for example, via antibody-dependent cell-mediated cytotoxicity (ADCC)). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for

example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or caricadic cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component (s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

ADMINISTRATION AND DOSING A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier.

Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable"means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient (s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-3, IL-5, IL-6, IL-7, IFN, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti- thrombotic factor, or agent.

A protein of the present invention may be active in multimers (e. g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein (s) of present invention along with protein or peptide antigens. The protein peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen (s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunolgobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or layers

in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U. S. Patent No. 4,235,871; U. S. Patent No. 4,501,728; U. S. Patent No. 4,837,028; and U. S. Patent No. 4,737,323, all of which are incorporated herein by reference.

As used herein, the term"therapeutically effective amount"means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i. e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either simultaneously with the cytokine (s), lymphokine (s), other hematopoietic factor (s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine (s), lymphokine (s), other hematopoietic factor (s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention.

When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution.

The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity,

stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 to about 100 mg (preferably about lng to about 10 mg, more preferably about 0.1 to about 1 mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. As used herein, the term"antibody"includes antibody, a chimeric antibody, a single-chain antibody, a CDR-grafted antibody, a humanized antibody, or fragments thereof which bind to the indicated protein. Such term also includes any other species derived from an antibody or antibody sequence which is capable of binding the indicated protein.

Antibodies to a particular protein can be produced by methods well known to those skilled in the art. For example, monoclonal antibodies can be produced by generation of antibody-producing hybridomas in accordance with known methods (see for example, Goding, 1983, Monoclonal antibodies: principles and practice, Academic Press Inc., New York; and 1992,"Production of Monoclonal Antibodies"in Current Protocols in Immunology, Unit 2.5, Greene Publishing Assoc. and John Wiley & Sons). Polyclonal sera and antibodies can be produced by inoculation of a mammalian subject with the relevant protein or fragments thereof in accordance with known methods. Fragments of antibodies, receptors, or other reactive peptides can be produced from the corresponding antibodies by cleavage of and collection of the desired fragments in accordance with known methods (see for example, Goding, supra; and Andrew et al., 1992,"Fragmentation of Current Protocols in Immunology, Unit 2.8, Greene Publishing Assoc. and John Wiley & Sons). Chimeric antibodies and single chain antibodies can also be produced in accordance with known recombinant methods (see for example, 5,169,939, 5,194,594, and 5,576,184). Humanized antibodies can also be made from corresponding murine antibodies in accordance with well known methods (see for example, U. S. Patent Nos. 5,530,101,5,585,089, and 5,693,762). Additionally, human antibodies may be produced in non-human animals such as mice that have been genetically altered to express human antibody molecules (see for example Fishwild et 1996, Nature Biotechnology 14: Mendez et al., 1997, Nature Genetics 15: 146-156 (erratum Nature Genetics 16: 410); and U. S. Patents 5,877,397 and 5,625,126). Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin

(KLH). Methods for synthesizing such peptides are known in the art, for example, as in R. P. Merrifield, J.

Amer. Chem. Soc. 85,2149-2154 (1963); J. L. Krstenansky, et FEBS Lett. 211,10 (1987).

Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and materials such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxapatite, bioglass, aluminates,

Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate.

The may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

Presently preferred is a 50: 50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns.

In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl- methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents

include hyaluronic acid, sodium alginate, poly (ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly (vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorbtion of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor platelet derived growth factor (PDGF), transforming growth factors and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e. g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e. g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage.

Progress can be monitored by periodic assessment of growth repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells.

Treated cells can then be introduced in vivo for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

What is claimed is: An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID NO: 1; (b) the nucleotide sequence of SEQ ID NO: from nucleotide 27 to nucleotide 260; (c) the nucleotide sequence of SEQ ID 1 from nucleotide 72 to nucleotide 260; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number 207114; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number 207114; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number 207114; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number 207114; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 2; (i) a nucleotide sequence encoding a protein

comprising a fragment of the amino acid sequence of SEQ ID 2, the fragment comprising eight contiguous amino acids of SEQ ID 2; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID NO:

2. The polynucleotide of claim 1 wherein said polynucleotide is operably linked to at least one expression control sequence.

3. A host cell transformed with the polynucleotide of claim 2.

4. The host cell of claim 3, wherein said cell is a mammalian cell.

5. A process for producing a protein encoded by the polynucleotide of claim 2, which process comprises: (a) growing a culture of a host cell in a suitable culture medium, wherein the host cell has been transformed with the polynucleotide of claim 2; and (b) purifying said protein from the culture.

6. A protein produced according to the process of claim 5.

7. An isolated polynucleotide encoding the protein of claim 6.

8. The polynucleotide of claim 7, wherein the polynucleotide comprises the insert of clone deposited with the ATCC under accession number 207114.

9. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 2; (b) a fragment of the amino acid sequence of SEQ ID 2, the fragment comprising eight contiguous amino acids of SEQ ID 2; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number 207114; the protein being substantially free from other mammalian proteins.

10. The protein of claim 9, wherein said protein comprises the amino acid sequence of SEQ ID 2.

11. A composition comprising the protein of claim 9 and a pharmaceutically acceptable carrier.

12. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 3; (b) the nucleotide sequence of SEQ ID 3 from nucleotide 6 to nucleotide 1325; (c) the nucleotide sequence of SEQ ID 3 from nucleotide 99 to nucleotide 1325; (d) the nucleotide sequence of the full-length protein coding sequence of clone vpl0_1 deposited with the ATCC under accession number 207114; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone vpl0_1 deposited with the ATCC under accession number 207114; (f) the nucleotide sequence of a mature protein coding sequence of clone vpl0_1 deposited with the ATCC under accession number 207114; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number 207114; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 4; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 4, the fragment comprising eight contiguous amino acids of SEQ ID 4; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a

polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 3.

13. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 4; (b) a fragment of the amino acid sequence of SEQ ID 4, the fragment comprising eight contiguous amino acids of SEQ ID 4; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number 207114; the protein being substantially free from other mammalian proteins.

14. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 5; (b) the nucleotide sequence of SEQ ID from nucleotide 149 to nucleotide 322; (c) the nucleotide sequence of SEQ ID from nucleotide 200 to nucleotide 322; (d) the nucleotide sequence of the full-length protein coding sequence of clone vpl deposited with the ATCC under accession number 207114; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number 207114; the nucleotide sequence of a mature protein coding sequence of clone vpl deposited with the ATCC under accession number 207114; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone vpl deposited with the ATCC under accession number 207114; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 6; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 6, the fragment comprising eight contiguous amino acids of SEQ ID 6; conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 5.

15. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 6; (b) a fragment of the amino acid sequence of SEQ ID 6, the fragment comprising eight contiguous amino acids of SEQ ID 6; and the amino acid sequence encoded by the insert of clone vpl deposited with the ATCC under accession number 207114; the protein being substantially free from other mammalian proteins.

16. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 7; (b) the nucleotide sequence of SEQ ID 7 from nucleotide 288 to nucleotide 629; (c) the nucleotide sequence of SEQ ID 7 from nucleotide 363 to nucleotide 629; (d) the nucleotide sequence of the full-length protein coding sequence of clone vpl3_1 deposited with the ATCC under accession number 207114; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone vpl3_1 deposited with the ATCC under accession number 207114; (f) the nucleotide sequence of a mature protein coding sequence of clone vpl3_1 deposited with the ATCC under accession number 207114; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone vpl3_1 deposited with the ATCC under accession number 207114; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 8; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 8, the fragment comprising eight contiguous amino acids of SEQ ID 8; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 7.

17. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 8; (b) a fragment of the amino acid sequence of SEQ ID 8, the fragment comprising eight contiguous amino acids of SEQ ID 8; and the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number 207114; the protein being substantially free from other mammalian proteins.

18. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 9; (b) the nucleotide sequence of SEQ ID 9 from nucleotide 11 to nucleotide 298; (c) the nucleotide sequence of SEQ ID 9 from nucleotide 149 to nucleotide 298; (d) the nucleotide sequence of the full-length protein coding sequence of clone vpl6_1 deposited with the ATCC under accession number 207114; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone vpl6_1 deposited with the ATCC under accession number 207114; (f) the nucleotide sequence of a mature protein coding sequence of clone vpl6_1 deposited with the ATCC under accession number 207114; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number 207114; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO: 10; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 10, the fragment comprising eight contiguous amino acids of SEQ ID NO: 10; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 9.

19. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID NO: 10; (b) a fragment of the amino acid sequence of SEQ ID 10, the fragment comprising eight contiguous amino acids of SEQ ID 10; and (c) the amino acid sequence encoded by the insert of clone vpl6_1 deposited with the ATCC under accession number 207114; the protein being substantially free from other mammalian proteins.

20. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID NO: 11; (b) the nucleotide sequence of SEQ ID NO: 11 from nucleotide 257 to nucleotide 607; (c) the nucleotide sequence of SEQ ID NO: 11 from nucleotide 479 to nucleotide 607; (d) the nucleotide sequence of the full-length protein coding sequence of clone vp21_1 deposited with the ATCC under accession number 207114; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone vp21_1 deposited with the ATCC under accession number 207114; the nucleotide sequence of a mature protein coding sequence of clone vp21_1 deposited with the ATCC under accession number 207114; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone vp21_1 deposited with the ATCC under accession number 207114; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO: 12; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 12, the fragment comprising eight contiguous amino acids of SEQ ID NO: 12; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID NO:

21. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 12; (b) a fragment of the amino acid sequence of SEQ ID 12, the fragment comprising eight contiguous amino acids of SEQ ID 12; and (c) the amino acid sequence encoded by the

insert of clone vp21_1 deposited with the ATCC under accession number 207114; the protein being substantially free from other mammalian proteins.

22. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID NO: 13; (b) the nucleotide sequence of SEQ ID NO: 13 from nucleotide 163 to nucleotide 477; (c) the nucleotide sequence of SEQ ID NO: 13 from nucleotide 238 to nucleotide 477; (d) the nucleotide sequence of the full-length protein coding sequence of clone vp22_1 deposited with the ATCC under accession number 207114; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone vp22_1 deposited with the ATCC under accession number 207114; (f) the nucleotide sequence of a mature protein coding sequence of clone vp22_1 deposited with the ATCC under accession number 207114; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone vp22_1 deposited with the ATCC under accession number 207114; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO: 14; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 14, the fragment comprising eight contiguous amino acids of SEQ ID NO: 14; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 13.

23. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 14; (b) a fragment of the amino acid sequence of SEQ ID 14, the fragment comprising eight contiguous amino acids of SEQ ID NO: 14; and (c) the amino acid sequence encoded by the insert of clone vp22_1 deposited with the ATCC under accession number 207114; the protein being substantially free from other mammalian proteins.

24. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting (a) the nucleotide sequence of SEQ ID NO: 15; (b) the nucleotide sequence of SEQ ID NO: 15 from nucleotide 58 to nucleotide 624; (c) the nucleotide sequence of SEQ ID NO: 15 from nucleotide 106 to nucleotide 624; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number 207114; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone vq2_1 deposited with the ATCC under accession number 207114; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number 207114; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone vq2_1 deposited with the ATCC under accession number 207114; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 16; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 16, the fragment comprising eight contiguous amino acids of SEQ ID NO: 16; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide. sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID NO: 15.

25. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID NO: 16; (b) a fragment of the amino acid sequence of SEQ ID 16, the fragment comprising eight contiguous amino acids of SEQ ID NO: 16; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number 207114; the protein being substantially free from other mammalian proteins.

26. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 17; (b) the nucleotide sequence of SEQ ID NO: 17 from nucleotide 773 to nucleotide 1090; (c) the nucleotide sequence of SEQ ID NO: 17 from nucleotide 842 to nucleotide 1090; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number 207114; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone vq3_1 deposited with the ATCC under accession number 207114; (f) the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number 207114; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number 207114; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 18; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 18, the fragment comprising eight contiguous amino acids of SEQ ID NO: 18; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with formamide, to any one of the polynucleotides specified by and that has a length that is at least of the length of SEQ ID 17.

27. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID NO: 18; (b) a fragment of the amino acid sequence of SEQ ID 18, the fragment comprising eight contiguous amino acids of SEQ ID 18; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number 207114; the protein being substantially free from other mammalian proteins.

28. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 19; (b) the nucleotide sequence of SEQ ID 19 from nucleotide 96 to nucleotide 275; (c) the nucleotide sequence of SEQ ID NO: 19 from nucleotide 159 to nucleotide 275; (d) the nucleotide sequence of the full-length protein coding sequence of clone vq5_1 deposited with the ATCC under accession number 207114; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number 207114; the nucleotide sequence of a mature protein coding sequence of clone vq5_1 deposited with the ATCC under accession number 207114; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone vq5_1 deposited with the ATCC under accession number 207114; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 20; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 20, the fragment comprising eight contiguous amino acids of SEQ ID 20; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least of the length of SEQ ID 19.

29. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 20; (b) a fragment of the amino acid sequence of SEQ ID 20, the fragment comprising eight contiguous amino acids of SEQ ID 20; and (c) the amino acid sequence encoded by the insert of clone vq5_1 deposited with the ATCC under accession number 207114; the protein being substantially free from other mammalian proteins.

30. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting (a) the nucleotide sequence of SEQ ID (b) the nucleotide sequence of SEQ ID 21 from nucleotide 176 to nucleotide 340; (c) the nucleotide sequence of SEQ ID 21 from nucleotide 230 to nucleotide 340; (d) the

nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number 207114; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number 207114; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number 207114; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone vq6_1 deposited with the ATCC under accession number 207114; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 22; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 22, the fragment comprising eight contiguous amino acids of SEQ ID 22; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least of the length of SEQ ID

31. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 22; (b) a fragment of the amino acid sequence of SEQ ID 22, the fragment comprising eight contiguous amino acids of SEQ ID 22; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number 207114; the protein being substantially free from other mammalian proteins.

32. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting (a) the nucleotide sequence of SEQ ID 23; (b) the nucleotide sequence of SEQ ID 23 from nucleotide 29 to nucleotide 1111; (c) the nucleotide sequence of SEQ ID 23 from nucleotide 167 to nucleotide 1111; (d) the nucleotide sequence of the full-length protein coding sequence of clone vrl_1 deposited with the ATCC under accession number 207114; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone vrl_1 deposited with the ATCC under accession number 207114; (f) the nucleotide sequence of a mature protein coding sequence of clone vrl_1 deposited with the ATCC under accession number 207114; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone vrl_1 deposited with the ATCC under accession number 207114; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 24; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 24, the fragment comprising eight contiguous amino acids of SEQ ID 24; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 23.

33. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 24; (b) a fragment of the amino acid sequence of SEQ ID 24, the fragment comprising eight contiguous amino acids of SEQ ID 24; and (c) the amino acid sequence encoded by the insert of clone vrl_1 deposited with the ATCC under accession number 207114; the protein being substantially free from other mammalian proteins.

34. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 25; (b) the nucleotide sequence of SEQ ID 25 from nucleotide 13 to nucleotide 513; (c) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number 207115; (d) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number 207115; (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 26; a

nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 26, the fragment comprising eight contiguous amino acids of SEQ ID 26; (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)- (d); and (h) the nucleotide, sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least of the length of SEQ ID 25.

35. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 26; (b) a fragment of the amino acid sequence of SEQ ID 26, the fragment comprising eight contiguous amino acids of SEQ ID 26; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number 207115; the protein being substantially free from other mammalian proteins.

36. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 27; (b) the nucleotide sequence of SEQ ID 27 from nucleotide 79 to nucleotide 345; (c) the nucleotide sequence of SEQ ID 27 from nucleotide 130 to nucleotide 345; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 28; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 28, the fragment comprising eight contiguous amino acids of SEQ ID 28; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 27.

37. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 28; (b) a fragment of the amino acid sequence of SEQ ID 28, the fragment comprising eight contiguous amino acids of SEQ ID 28; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins.

An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 29; (b) the nucleotide sequence of SEQ ID 29 from nucleotide 72 to nucleotide 236; (c) the nucleotide sequence of SEQ ID 29 from nucleotide 150 to nucleotide 236; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 30; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 30, the fragment comprising eight contiguous amino acids of SEQ ID 30; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the

polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 29.

39. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 30; (b) a fragment of the amino acid sequence of SEQ ID 30, the fragment comprising eight contiguous amino acids of SEQ ID 30; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins.

40. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting (a) the nucleotide sequence of SEQ ID (b) the nucleotide sequence of SEQ ID 31 from nucleotide 135 to nucleotide 884; (c) the nucleotide sequence of SEQ ID 31 from nucleotide 183 to nucleotide 884; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 32; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 32, the fragment comprising eight contiguous amino acids of SEQ ID 32; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least of the length of SEQ ID

41. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 32; (b) a fragment of the amino acid sequence of SEQ ID 32, the fragment comprising eight contiguous amino acids of SEQ ID 32; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins.

42. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting (a) the nucleotide sequence of SEQ ID 33; (b) the nucleotide sequence of SEQ ID 33 from nucleotide 42 to nucleotide 206; (c) the nucleotide sequence of SEQ ID 33 from nucleotide 111 to nucleotide 206; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; (f) the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 34; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 34, the fragment comprising eight contiguous amino acids of SEQ ID 34; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least

of the length of SEQ ID 33.

43. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 34; (b) a fragment of the amino acid sequence of SEQ ID 34, the fragment comprising eight contiguous amino acids of SEQ ID 34; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins.

44. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 35; (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 35 from nucleotide 17 to nucleotide 253; a polynucleotide comprising the nucleotide sequence of SEQ ID 35 from nucleotide 98 to nucleotide 253; (d) a polynucleotide comprising the nucleotide sequence of the full- length protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (e) a polynucleotide encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (g) a polynucleotide encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA- 362; (h) a polynucleotide encoding a protein comprising the amino acid sequence 36; (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 36 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID 36; a polynucleotide which is an allelic variant of a polynucleotide of above; (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above; a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i); and (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)- (i) and that has a length that is at least 25% of the length of SEQ ID NO: 35.

45. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 36; (b) a fragment of the amino acid sequence of SEQ ID 36, the fragment comprising eight contiguous amino acids of SEQ ID 36; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins.

46. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 37; (b) the nucleotide sequence of SEQ ID 37 from nucleotide 68 to nucleotide 424; (c) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (d) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 38; a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 38, the fragment comprising eight contiguous amino acids of SEQ ID 38; (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)- (d); and (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 37.

47. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 38; (b) a fragment of the amino acid sequence of SEQ ID 38, the fragment comprising eight contiguous amino acids of SEQ ID 38; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the protein being

substantially free from other mammalian proteins.

48. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 39; (b) the nucleotide sequence of SEQ ID 39 from nucleotide 103 to nucleotide 261; (c) the nucleotide sequence of SEQ ID 39 from nucleotide 154 to nucleotide 261; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 40; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 40, the fragment comprising eight contiguous amino acids of SEQ ID 40; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 39.

49. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 40; (b) a fragment of the amino acid sequence of SEQ ID 40, the fragment comprising eight contiguous amino acids of SEQ ID 40; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins.

50. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID (b) the nucleotide sequence of SEQ ID 41 from nucleotide 1575 to nucleotide 3038; (c) the nucleotide sequence of SEQ ID 41 from nucleotide 1650 to nucleotide 3038; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 42; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 42, the fragment comprising eight contiguous amino acids of SEQ ID 42; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 41.

51. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 42; (b) a fragment of the amino acid sequence of SEQ ID 42, the fragment comprising eight contiguous amino acids of SEQ ID 42; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins.

52. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting (a)

the nucleotide sequence of SEQ ID 43; (b) the nucleotide sequence of SEQ ID 43 from nucleotide 2112 to nucleotide 2363; (c) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (d) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 44; the amino acid sequence of SEQ ID 44, the fragment comprising eight contiguous amino acids of SEQ ID 44; (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)- (d); and (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 43.

53. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 44; (b) a fragment of the amino acid sequence of SEQ ID 44, the fragment comprising eight contiguous amino acids of SEQ ID 44; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins.

54. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 45; (b) the nucleotide sequence of SEQ ID 45 from nucleotide 36 to nucleotide 707; the nucleotide sequence of SEQ ID 45 from nucleotide 393 to nucleotide 707; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; (f) the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 46; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 46, the fragment comprising eight contiguous amino acids of SEQ ID 46; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 45.

55. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 46; (b) a fragment of the amino acid sequence of SEQ ID 46, the fragment comprising eight contiguous amino acids of SEQ ID 46; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins.

56. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 47; (b) the nucleotide sequence of SEQ ID 47 from nucleotide 74 to nucleotide 295; (c) the nucleotide sequence of SEQ ID 47 from nucleotide 134 to nucleotide 295; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone

deposited with the ATCC under accession number PTA-362; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 48; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 48, the fragment comprising eight contiguous amino acids of SEQ ID 48; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 47.

57. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 48; (b) a fragment of the amino acid sequence of SEQ ID 48, the fragment comprising eight contiguous amino acids of SEQ ID 48; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins.

58. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting (a) the nucleotide sequence of SEQ ID 49; (b) the nucleotide sequence of SEQ ID 49 from nucleotide 45 to nucleotide 383; (c) the nucleotide sequence of SEQ ID 49 from nucleotide 312 to nucleotide 383; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 50; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 50, the fragment comprising eight contiguous amino acids of SEQ ID 50; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 49.

59. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 50; (b) a fragment of the amino acid sequence of SEQ ID 50, the fragment comprising eight contiguous amino acids of SEQ ID 50; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins.

60. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID (b) the nucleotide sequence of SEQ ID 51 from nucleotide 186 to nucleotide 1739; (c) the nucleotide sequence of SEQ ID 51 from nucleotide 288 to nucleotide 1739; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-362; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-362; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 52; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 52, the fragment comprising eight contiguous amino acids of

SEQ ID 52; conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID

61. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 52; (b) a fragment of the amino acid sequence of SEQ ID 52, the fragment comprising eight contiguous amino acids of SEQ ID 52; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins.

62. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 53; (b) the nucleotide sequence of SEQ ID 53 from nucleotide 440 to nucleotide 835; (c) the nucleotide sequence of SEQ ID 53 from nucleotide 632 to nucleotide 835; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; (f) the nucleotide sequence of a mature protein coding sequence of clone vol deposited with the ATCC under accession number PTA-366; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone vol deposited with the ATCC under accession number PTA-366; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 54; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 54, the fragment comprising eight contiguous amino acids of SEQ ID 54; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 53.

63. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 54; (b) a fragment of the amino acid sequence of SEQ ID 54, the fragment comprising eight contiguous amino acids of SEQ ID 54; and (c) the amino acid sequence encoded by the insert of clone vol deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins.

64. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 55; (b) the nucleotide sequence of SEQ ID 55 from nucleotide 72 to nucleotide 329; (c) the nucleotide sequence of SEQ ID 55 from nucleotide 120 to nucleotide 329; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 56; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 56, the fragment comprising eight contiguous amino acids of SEQ ID 56; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C

with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 55.

65. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 56; (b) a fragment of the amino acid sequence of SEQ ID 56, the fragment comprising eight contiguous amino acids of SEQ ID 56; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins.

66. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 57; (b) the nucleotide sequence of SEQ ID 57 from nucleotide 227 to nucleotide 439; (c) the nucleotide sequence of SEQ ID 57 from nucleotide 287 to nucleotide 439; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 58; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 58, the fragment comprising eight contiguous amino acids of SEQ ID 58; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 57.

67. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 58; (b) a fragment of the amino acid sequence of SEQ ID 58, the fragment comprising eight contiguous amino acids of SEQ ID 58; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins.

68. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 59; (b) the nucleotide sequence of SEQ ID 59 from nucleotide 96 to nucleotide 341; (c) the nucleotide sequence of SEQ ID 59 from nucleotide 174 to nucleotide 341; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; (f) the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 60; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 60, the fragment comprising eight contiguous amino acids of SEQ ID 60; (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 59.

69. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 60; (b) a fragment the amino acid sequence of SEQ ID 60, the fragment comprising eight contiguous amino acids of SEQ ID 60; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins.

70. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting (a) the nucleotide sequence of SEQ ID (b) the nucleotide sequence of SEQ ID 61 from nucleotide 90 to nucleotide 599; (c) the nucleotide sequence of SEQ ID 61 from nucleotide 165 to nucleotide 599; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 62; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 62, the fragment comprising eight contiguous amino acids of SEQ ID 62; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 61.

71. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 62; (b) a fragment of the amino acid sequence of SEQ ID 62, the fragment comprising eight contiguous amino acids of SEQ ID 62; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins.

72. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting (a) the nucleotide sequence of SEQ ID 63; (b) the nucleotide sequence of SEQ ID 63 from nucleotide 209 to nucleotide (c) the nucleotide sequence of SEQ ID 63 from nucleotide 398 to nucleotide (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 64; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID the fragment comprising eight contiguous amino acids of SEQ ID 64; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least of the length of SEQ ID 63.

73. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 64; (b) a fragment of the amino acid sequence of SEQ ID 64, the fragment comprising eight contiguous amino acids of SEQ ID 64; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the protein being

substantially free from other mammalian proteins.

74. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 65; (b) the nucleotide sequence of SEQ ID 65 from nucleotide 31 to nucleotide (c) the nucleotide sequence of SEQ ID 65 from nucleotide 97 to nucleotide (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 66; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 66, the fragment comprising eight contiguous amino acids of SEQ ID 66; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 65.

75. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 66; (b) a fragment of the amino acid sequence of SEQ ID 66, the fragment comprising eight contiguous amino acids of SEQ ID 66; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins.

76. An isolated polynucleotide comprising sequence selected from the group consisting (a) the nucleotide sequence of SEQ ID 67; (b) the nucleotide sequence of SEQ ID 67 from nucleotide 23 to nucleotide 736; (c) the nucleotide sequence of SEQ ID 67 from nucleotide 83 to nucleotide 736; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 68; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 68, the fragment comprising eight contiguous amino acids of SEQ ID 68; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 67.

77. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 68; (b) a fragment the amino acid sequence of SEQ ID 68, the fragment comprising eight contiguous amino acids of SEQ ID 68; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins.

78. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID 69; (b) the nucleotide sequence of SEQ ID 69 from nucleotide 104 to nucleotide 1399; (c) the nucleotide sequence of SEQ ID 69 from nucleotide 158 to nucleotide 1399; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 70; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 70, the fragment comprising eight contiguous amino acids of SEQ ID 70; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 69.

79. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 70; (b) a fragment of the amino acid sequence of SEQ ID 70, the fragment comprising eight contiguous amino acids of SEQ ID 70; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins.

80. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting (a) the nucleotide sequence of SEQ ID 71; (b) the nucleotide sequence of SEQ ID 71 from nucleotide 174 to nucleotide 1595; (c) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (d) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 72; a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 72, the fragment comprising eight contiguous amino acids of SEQ ID 72; (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)- (d); and (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least of the length of SEQ ID

81. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 72; (b) a fragment of the amino acid sequence of SEQ ID 72, the fragment comprising eight contiguous amino acids of SEQ ID 72; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins.

82. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 73; (b) the nucleotide sequence of SEQ ID 73 from nucleotide 129 to nucleotide 311; (c) the nucleotide sequence of SEQ ID 73 from nucleotide 195 to nucleotide 311; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone

deposited with the ATCC under accession number PTA-366; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 74; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 74, the fragment comprising eight contiguous amino acids of SEQ ID 74; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 73.

83. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 74; (b) a fragment of the amino acid sequence of SEQ ID 74, the fragment comprising eight contiguous amino acids of SEQ ID 74; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins.

84. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 75; (b) the nucleotide sequence of SEQ ID 75 from nucleotide 73 to nucleotide 798; (c) the nucleotide sequence of SEQ ID 75 from nucleotide 142 to nucleotide 798; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 76; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 76, the fragment comprising eight contiguous amino acids of SEQ ID 76; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 75.

85. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 76; (b) a fragment of the amino acid sequence of SEQ ID 76, the fragment comprising eight contiguous amino acids of SEQ ID 76; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins.

86. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide. sequence of SEQ ID 27; (b) the nucleotide sequence of SEQ ID 27 from nucleotide 26 to nucleotide 307; (c) the nucleotide sequence of SEQ ID 27 from nucleotide 101 to nucleotide 307; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-366; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-366; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 78; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 78, the fragment comprising eight

contiguous amino acids of SEQ ID 78; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 27.

87. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 78; (b) a fragment of the amino acid sequence of SEQ ID 78, the fragment comprising eight contiguous amino acids of SEQ ID 78; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins.

88. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting (a) the nucleotide sequence of SEQ ID 79; (b) the nucleotide sequence of SEQ ID 79 from nucleotide 43 to nucleotide 228; (c) the nucleotide sequence of SEQ ID 79 from nucleotide 94 to nucleotide 228; (d) the nucleotide sequence of the full-length protein coding sequence of clone vp23_1 deposited with the ATCC under accession number PTA-368; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone vp23_1 deposited with the ATCC under accession number PTA-368; the nucleotide sequence of a mature protein coding sequence of clone vp23_1 deposited with the ATCC under accession number PTA-368; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 80; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 80, the fragment comprising eight contiguous amino acids of SEQ ID 80; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 79.

89. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 80; (b) a fragment of the amino acid sequence of SEQ ID 80, the fragment comprising eight contiguous amino acids of SEQ ID 80; and (c) the amino acid sequence encoded by the insert of clone vp23_1 deposited with the ATCC under accession number PTA-368; the protein being substantially free from other mammalian proteins.

90. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting (a) the nucleotide sequence of SEQ ID (b) the nucleotide sequence of SEQ ID 81 from nucleotide 245 to nucleotide 427; (c) the nucleotide sequence of SEQ ID 81 from nucleotide 308 to nucleotide 427; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; (f) the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 82; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 82, the fragment comprising eight contiguous amino acids of SEQ ID 82; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, SSC degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under

conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 81.

91. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 82; (b) a fragment of the amino acid sequence of SEQ ID 82, the fragment comprising eight contiguous amino acids of SEQ ID 82; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-368; the protein being substantially free from other mammalian proteins.

92. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 83; (b) the nucleotide sequence of SEQ ID 83 from nucleotide 119 to nucleotide 475; (c) the nucleotide sequence of SEQ ID 83 from nucleotide 185 to nucleotide 475; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; (f) the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 84; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 84, the fragment comprising eight contiguous amino acids of SEQ ID 84; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 83.

93. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 84; (b) a fragment of the amino acid sequence of SEQ ID 84, the fragment comprising eight contiguous amino acids of SEQ ID 84; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-368; the protein being substantially free from other mammalian proteins.

94. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting (a) the nucleotide sequence of SEQ ID 85; (b) the nucleotide sequence of SEQ ID 85 from nucleotide 90 to nucleotide 323; (c) the nucleotide sequence of SEQ ID 85 from nucleotide 141 to nucleotide 323; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone vq9_l deposited with the ATCC under accession number PTA-368; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 86; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 86, the fragment comprising eight contiguous amino acids of SEQ ID 86; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 85.

95. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 86; (b) a fragment of the amino acid sequence of SEQ ID 86, the fragment comprising eight contiguous amino acids of SEQ ID 86; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-368; the protein being substantially free from other mammalian proteins.

96. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 87; (b) the nucleotide sequence of SEQ ID 87 from nucleotide 18 to nucleotide 452; (c) the nucleotide sequence of SEQ ID 87 from nucleotide 72 to nucleotide 452; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; (f) the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 88; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 88, the fragment comprising eight contiguous amino acids of SEQ ID 88; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 87.

97. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 88; (b) a fragment of the amino acid sequence of SEQ ID 88, the fragment comprising eight contiguous amino acids of SEQ ID 88; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-368; the protein being substantially free from other mammalian proteins.

98. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 89; (b) the nucleotide sequence of SEQ ID 89 from nucleotide 196 to nucleotide 378; (c) the nucleotide sequence of SEQ ID 89 from nucleotide 262 to nucleotide 378; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 90; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 90, the fragment comprising eight contiguous amino acids of SEQ ID 90; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or4X SSC degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 89.

99. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 90; (b) a fragment of the amino acid sequence of SEQ ID 90, the fragment comprising eight contiguous amino acids of SEQ ID 90; and (c) the amino acid sequence encoded by the

insert of clone deposited with the ATCC under accession number PTA-368; the protein being substantially free from other mammalian proteins.

100. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 91; (b) the nucleotide sequence of SEQ ID 91 from nucleotide 35 to nucleotide 718; (c) the nucleotide sequence of SEQ ID 91 from nucleotide 173 to nucleotide 718; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; (f) the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 92; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 92, the fragment comprising eight contiguous amino acids of SEQ ID 92; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, SSC degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 91.

101. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 92; (b) a fragment of the amino acid sequence of SEQ ID 92, the fragment comprising eight contiguous amino acids of SEQ ID 92; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-368; the protein being substantially free from other mammalian proteins.

102. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide. sequence of SEQ ID 93; (b) the nucleotide sequence of SEQ ID 93 from nucleotide 1 to nucleotide 762; (c) the nucleotide sequence of SEQ ID 93 from nucleotide 70 to nucleotide 762; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; (f) the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 94; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 94, the fragment comprising eight contiguous amino acids of SEQ ID 94; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 93.

103. A protein comprising an amino acid sequence selected from the group consisting (a) the amino acid sequence of SEQ ID 94; (b) a fragment of the amino acid sequence of SEQ ID 94, the fragment comprising eight contiguous amino acids of SEQ ID 94; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-368; the protein being substantially free from other mammalian proteins.

104. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting (a) the nucleotide sequence of SEQ ID 95; (b) the nucleotide sequence of SEQ ID 95 from nucleotide 106 to nucleotide 792; (c) the nucleotide sequence of SEQ ID 95 from nucleotide 172 to nucleotide 792; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; (f) the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 96; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 96, the fragment comprising eight contiguous amino acids of SEQ ID 96; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 95.

105. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 96; (b) a fragment of the amino acid sequence of SEQ ID 96, the fragment comprising eight contiguous amino acids of SEQ ID 96; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-368; the protein being substantially free from other mammalian proteins.

106. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting (a) the nucleotide sequence of SEQ ID 97; (b) the nucleotide sequence of SEQ ID 97 from nucleotide 40 to nucleotide 315; (c) the nucleotide sequence of SEQ ID 97 from nucleotide 124 to nucleotide 315; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 98; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID the fragment comprising eight contiguous amino acids of SEQ ID 98; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 97.

107. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 98; (b) a fragment of the amino acid sequence of SEQ ID 98, the fragment comprising eight contiguous amino acids of SEQ ID 98; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-368; the protein being substantially free from other mammalian proteins.

108. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 99; (b) the nucleotide sequence of SEQ ID 99 from nucleotide 70 to nucleotide 699; (c) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-368; (d) a nucleotide sequence encoding the

full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-368; (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 100; a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 100, the fragment comprising eight contiguous amino acids of SEQ ID 100; (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)- (d); and (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 99.

109. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID NO: 100; (b) a fragment of the amino acid sequence of SEQ ID 100, the fragment comprising eight contiguous amino acids of SEQ ID 100; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-368; the protein being substantially free from other mammalian proteins.

110. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID NO: (b) the nucleotide sequence of SEQ ID 101 from nucleotide 170 to nucleotide 394; (c) the nucleotide sequence of SEQ ID from nucleotide 227 to nucleotide 394; (d) the nucleotide sequence of the full-length protein coding sequence of clone PTA-1075 deposited with the ATCC under accession number PTA-1075; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; (f) the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 102; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 102, the fragment comprising eight contiguous amino acids of SEQ ID NO: 102; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID NO: 101.

111. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 102; (b) a fragment of the amino acid sequence of SEQ ID 102, the fragment comprising eight contiguous amino acids of SEQ ID 102; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; the protein being substantially free from other mammalian proteins.

112. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting (a) the nucleotide. sequence of SEQ ID NO: 103; (b) the nucleotide sequence of SEQ ID NO: 103 from nucleotide 43 to nucleotide 198; (c) the nucleotide sequence of SEQ ID NO: 103 from nucleotide 85 to nucleotide 198; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; (f) the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO: 104; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 104, the fragment

comprising eight contiguous amino acids of SEQ ID 104; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 103.

113. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 104; (b) a fragment the amino acid sequence of SEQ ID 104, the fragment comprising eight contiguous amino acids of SEQ ID 104; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; the protein being substantially free from other mammalian proteins.

114. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID NO: 105; (b) the nucleotide sequence of SEQ ID 105 from nucleotide 260 to nucleotide 1552; (c) the nucleotide sequence of SEQ ID NO: 105 from nucleotide 335 to nucleotide 1552; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO: 106; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 106, the fragment comprising eight contiguous amino acids of SEQ ID 106; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID NO: 105.

115. A protein comprising an amino acid sequence selected from the group consisting (a) the amino acid sequence of SEQ ID 106; (b) a fragment of the amino acid sequence of SEQ ID 106, the fragment comprising eight contiguous amino acids of SEQ ID NO: 106; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; the protein being substantially free from other mammalian proteins.

116. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID NO: 107; (b) the nucleotide sequence of SEQ ID NO: 107 from nucleotide 15 to nucleotide 320; (c) the nucleotide sequence of SEQ ID NO: 107 from nucleotide 72 to nucleotide 320; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone vo31_1 deposited with the ATCC under accession number PTA-1075; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO: 108; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 108, the fragment comprising eight contiguous amino acids of SEQ ID 108; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide

sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID NO: 107.

117. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 108; (b) a fragment of the amino acid sequence of SEQ ID 108, the fragment comprising eight contiguous amino acids of SEQ ID NO: 108; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; the protein being substantially free from other mammalian proteins.

118. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 109; (b) the nucleotide sequence of SEQ ID NO: 109 from nucleotide 38 to nucleotide 1255; (c) the nucleotide sequence of SEQ ID NO: 109 from nucleotide 86 to nucleotide 1255; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; (f) the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO: 110; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 110, the fragment comprising eight contiguous amino acids of SEQ ID NO: 110; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, SSC at 42 degrees C with formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 109.

119. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID NO: 110; (b) a fragment of the amino acid sequence of SEQ ID 110, the fragment comprising eight contiguous amino acids of SEQ ID and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; the protein being substantially free from other mammalian proteins.

120. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting (a) the nucleotide sequence of SEQ ID NO: 111; (b) the nucleotide sequence of SEQ ID NO: 111 from nucleotide 80 to nucleotide 1276; (c) the nucleotide sequence of SEQ ID NO: 111 from nucleotide 131 to nucleotide 1276; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; (f) the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO: 112; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 112, the fragment comprising eight contiguous amino acids of SEQ ID NO: 112; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID NO:

121. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID NO: 112; (b) a fragment of the amino acid sequence of SEQ ID 112, the fragment comprising eight contiguous amino acids of SEQ ID NO: 112; and (c) the amino acid sequence encoded by the insert of clone vo33_1 deposited with the ATCC under accession number PTA-1075; the protein being substantially free from other mammalian proteins.

122. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID NO: 113; (b) the nucleotide sequence of SEQ ID NO: 113 from nucleotide 202 to nucleotide 429; (c) the nucleotide sequence of SEQ ID NO: 113 from nucleotide 292 to nucleotide 429; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 114; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 114, the fragment comprising eight contiguous amino acids of SEQ ID 114; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 113.

123. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID NO: 114; (b) a fragment of the amino acid sequence of SEQ ID NO: the fragment comprising eight contiguous amino acids of SEQ ID 114; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; the protein being substantially free from other mammalian proteins.

124. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting (a) the nucleotide sequence of SEQ ID NO: 115; (b) the nucleotide sequence of SEQ ID 115 from nucleotide 37 to nucleotide 1113; (c) the nucleotide sequence of SEQ ID NO: 115 from nucleotide 88 to nucleotide 1113; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone vq24_1 deposited with the ATCC under accession number PTA-1075; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 116; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 116, the fragment comprising eight contiguous amino acids of SEQ ID NO: 116; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID NO: 115.

125. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID NO: 116; (b) a fragment of the amino acid sequence of SEQ ID 116, the fragment comprising eight contiguous amino acids of SEQ ID NO: 116; and (c) the amino acid sequence

encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; the protein being substantially free from other mammalian proteins.

126. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence of SEQ ID 117; (b) the nucleotide sequence of SEQ ID NO: 117 from nucleotide 40 to nucleotide 207; (c) the nucleotide sequence of SEQ ID NO: 117 from nucleotide 103 to nucleotide 207; (d) the nucleotide sequence of the full-length protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (e) a nucleotide sequence encoding the full-length protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; the nucleotide sequence of a mature protein coding sequence of clone deposited with the ATCC under accession number PTA-1075; (g) a nucleotide sequence encoding a mature protein encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID 118; (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID 118, the fragment comprising eight contiguous amino acids of SEQ ID NO: 118; the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by and (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with formamide, to any one of the polynucleotides specified by and that has a length that is at least 25% of the length of SEQ ID 117.

127. A protein comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of SEQ ID 118; (b) a fragment of the amino acid sequence of SEQ ID 118, the fragment comprising eight contiguous amino acids of SEQ ID 118; and (c) the amino acid sequence encoded by the insert of clone deposited with the ATCC under accession number PTA-1075; the protein being substantially free from other mammalian proteins.